

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 11:17:50 ; Search time 4940 Seconds
(without alignments)
11064.268 Million cell updates/sec

Title: US-10-658-180-246

Perfect score: 1128
Sequence: 1 tcgaggaagaagagagctgaa.....tgcttcattagtaacgag 1128

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:1*
1: gb ba:*
2: gb _ntg:*
3: gb _in:*
4: gb _om:*
5: gb _ov:*
6: gb _pat:*
7: gb _ph:*
8: gb _pl:*
9: gb _pr:*
10: gb _ro:*
11: gb _sts:*
12: gb _sy:*
13: gb _un:*
14: gb _vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1128 | 100.0 | 1128 | 6 | AR412266 Sequence |
| 2 | 1128 | 100.0 | 1128 | 6 | AX193968 Sequence |
| 3 | 1036.2 | 91.9 | 1128 | 6 | AR412275 Sequence |
| 4 | 1036.2 | 91.9 | 1128 | 6 | AX193980 Sequence |
| 5 | 963.4 | 85.4 | 1128 | 6 | AR412269 Sequence |
| 6 | 963.4 | 85.4 | 1128 | 6 | AX193972 Sequence |
| 7 | 909 | 80.6 | 1128 | 6 | AR412272 Sequence |
| 8 | 909 | 80.6 | 1128 | 6 | AX193976 Sequence |
| 9 | 879 | 77.9 | 1128 | 6 | AR412278 Sequence |
| 10 | 879 | 77.9 | 1128 | 6 | AX193984 Sequence |
| 11 | 672.2 | 59.6 | 1138 | 6 | AR412253 Sequence |
| 12 | 672.2 | 59.6 | 1138 | 6 | AX193727 Sequence |
| 13 | 671.4 | 59.5 | 1158 | 6 | AR412250 Sequence |
| 14 | 671.4 | 59.5 | 1158 | 6 | AX193723 Sequence |
| 15 | 671.4 | 59.5 | 1161 | 6 | AR412288 Sequence |
| 16 | 671.4 | 59.5 | 1161 | 6 | AX194007 Sequence |
| 17 | 652.4 | 57.8 | 1167 | 6 | AX033231 Solanum c |
| 18 | 652.4 | 57.8 | 1167 | 6 | AR412284 Sequence |
| 19 | 652.4 | 57.8 | 1167 | 6 | AX193992 Sequence |

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|----|-------|------|------|---|-----------|---------------------|
| 20 | 619.8 | 54.9 | 1390 | 8 | SBUD09331 | U09331 Solanum bre |
| 21 | 618.2 | 54.8 | 1437 | 8 | STRNA01 | X01125 Potato mRNA |
| 22 | 616 | 54.6 | 1167 | 6 | AR412287 | AR412287 Sequence |
| 23 | 616 | 54.6 | 1167 | 6 | AX193996 | AX193996 Sequence |
| 24 | 610.2 | 54.1 | 1357 | 8 | STPOTAX | Z27221 S. tuberosum |
| 25 | 608.4 | 53.9 | 1339 | 6 | AR002974 | AR002974 Sequence |
| 26 | 608 | 53.9 | 1378 | 8 | STPATB2 | X13178 Potato mRNA |
| 27 | 608 | 53.9 | 1380 | 6 | AR002973 | AR002973 Sequence |
| 28 | 600 | 53.2 | 1354 | 8 | STPATB1 | X13179 Potato mRNA |
| 29 | 600 | 53.2 | 1404 | 8 | POTPATB | M21879 Potato patA |
| 30 | 595 | 52.7 | 1405 | 8 | AP498099 | AP498099 Solanum c |
| 31 | 390.6 | 34.6 | 1158 | 6 | AR412279 | AR412279 Sequence |
| 32 | 390.6 | 34.6 | 1158 | 6 | AX193986 | AX193986 Sequence |
| 33 | 380.2 | 33.7 | 1440 | 8 | NTU68484 | U68484 Nicotiana t |
| 34 | 210.2 | 18.6 | 1506 | 6 | AX298155 | AX298155 Sequence |
| 35 | 210.2 | 18.6 | 1506 | 8 | AP158027 | AP158027 Nicotiana |
| 36 | 198 | 17.6 | 5313 | 8 | STPATG | X03932 Solanum tub |
| 37 | 190 | 16.8 | 4029 | 8 | POTPATB | M18860 Potato patA |
| 38 | 190 | 16.8 | 6094 | 8 | STPATG1 | X03956 Potato (tet |
| 39 | 186.2 | 16.5 | 1577 | 8 | AP193067 | AP193067 Vigna ung |
| 40 | 185.6 | 16.5 | 1505 | 6 | AP158253 | AP158253 Nicotiana |
| 41 | 185.6 | 16.5 | 1509 | 6 | AX298159 | AX298159 Sequence |
| 42 | 185.2 | 16.4 | 276 | 6 | AR340167 | AR340167 Sequence |
| 43 | 185.2 | 16.4 | 276 | 6 | AX033682 | AX033682 Sequence |
| 44 | 181.6 | 16.1 | 1633 | 6 | AX146911 | AX146911 Sequence |
| 45 | 178.8 | 15.9 | 7373 | 8 | STPATP2 | X04078 Potato patA |

ALIGNMENTS

| | | | | | | |
|---|---|---|---------|-----|--------|-----------------|
| RESULT 1 | AR412266 | Sequence 246 from patent US 6639054. | 1128 bp | DNA | linear | PAT 18-DEC-2003 |
| LOCUS | AR412266 | Sequence 246 from patent US 6639054. | 1128 bp | DNA | linear | PAT 18-DEC-2003 |
| DEFINITION | AR412266 | Sequence 246 from patent US 6639054. | 1128 bp | DNA | linear | PAT 18-DEC-2003 |
| ACCESSION | AR412266 | Sequence 246 from patent US 6639054. | 1128 bp | DNA | linear | PAT 18-DEC-2003 |
| VERSION | AR412266.1 | GI:40167064 | 1128 bp | DNA | linear | PAT 18-DEC-2003 |
| KEYWORDS | Unknown. | | | | | |
| SOURCE | Unknown. | | | | | |
| ORGANISM | Unknown. | | | | | |
| REFERENCE | 1 (bases 1 to 1128) | | | | | |
| AUTHORS | Alibhai,M.F., Astwood,J.D., McPherson,C.A. and Sampson,H.A. | | | | | |
| TITLE | Preparation of deaerogenized proteins and permutenes | | | | | |
| JOURNAL | Patent: US 6639054-A 246 28-OCT-2003; | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| source | 1..1128 | | | | | |
| ORIGIN | /organism="unknown" | | | | | |
| | /mol_type="genomic DNA" | | | | | |
| Query Match | 100.0%; Score 1128; DB 6; Length 1128; | | | | | |
| Best Local Similarity | 100.0%; Pred. No. 1e-221; | | | | | |
| Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | |
| QY | 1 | TCGAGAAAAGAGGCTGAGCTTCATTTGAATTAACAAAATGCTGCTGCATTAAG | 60 | | | |
| DB | 1 | TCGAGAAAAGAGGCTGAGCTTCATTTGAATTAACAAAATGCTGCTGCATTAAG | 60 | | | |
| QY | 61 | GCACGTGCACTACTCTTCAGATTGATTAACATATACAGCAAGAGGAGCTGCTGGA | 120 | | | |
| DB | 61 | GCACGTGCACTACTCTTCAGATTGATTAACATATACAGCAAGAGGAGCTGCTGGA | 120 | | | |
| QY | 121 | CTGCTGACATTCAGATTTAGTATACAGAAAATGACTGATGACAGAGTTCTTACATGA | 180 | | | |
| DB | 121 | CTGCTGACATTCAGATTTAGTATACAGAAAATGACTGATGACAGAGTTCTTACATGA | 180 | | | |
| QY | 181 | CTGATTTATACCTTTTACAGCTTTTCAAGCTCTGATTCAGAAATTAACCTCAGGG | 240 | | | |
| DB | 181 | CTGATTTATACCTTTTACAGCTTTTCAAGCTCTGATTCAGAAATTAACCTCAGGG | 240 | | | |
| QY | 241 | TTCAAGAAAATGATTAACAGGACATCTGAAATGATGATGCTTCTGAGGCTATAA | 300 | | | |

| | | | | | | |
|----|------|----------------------|-------------------|------------------------|------------------------|------|
| Db | 241 | TTCAAGAAAAATGCAATTAA | CAGGCA | CAACTACTGAAATG | ATGATGCTTCTGAGGCTAATA | 300 |
| Qy | 301 | TGGAATTTATGTAC | AGTTGGTGA | AAAACTTAT | TGAAAGAAACCA | 360 |
| Db | 301 | TGGAATTTATGTAC | AGTTGGTGA | AAAACTTAT | TGAAAGAAACCA | 360 |
| Qy | 361 | CTGAACCTATAG | AGAAAGCTCTAA | AGAGTTTGCAAAAT | TGCTCTGATAG | 420 |
| Db | 361 | CTGAACCTATAG | AGAAAGCTCTAA | AGAGTTTGCAAAAT | TGCTCTGATAG | 420 |
| Qy | 421 | TCCGAGCAAA | CAAAAGCTTCTTAT | TGACCAAGAC | CAAGTTGGAGAAATG | 480 |
| Db | 421 | TCCGAGCAAA | CAAAAGCTTCTTAT | TGACCAAGAC | CAAGTTGGAGAAATG | 480 |
| Qy | 481 | GTAATTGATGAG | AGGTGGAATTTAG | AGGAGATCA | TTCCGGCTACATCTCGAAT | 540 |
| Db | 481 | GTAATTGATGAG | AGGTGGAATTTAG | AGGAGATCA | TTCCGGCTACATCTCGAAT | 540 |
| Qy | 541 | GACAACTTCAG | AAATGACATATATG | CAGATGCAAGACTTGCAGATTA | CTTGTGATGTA | 600 |
| Db | 541 | GACAACTTCAG | AAATGACATATATG | CAGATGCAAGACTTGCAGATTA | CTTGTGATGTA | 600 |
| Qy | 601 | TTGAGAGAA | CAAGTACAGAGGTTTAT | TGACTGCTATGATTA | AGTACTCCAAT | 660 |
| Db | 601 | TTGAGAGAA | CAAGTACAGAGGTTTAT | TGACTGCTATGATTA | AGTACTCCAAT | 660 |
| Qy | 661 | ATGCACCTTGTG | CTGCTCCCAAGAAAT | TTGTACCTTTTACTTGGAA | CATGAGCCCTCAGA | 720 |
| Db | 661 | ATGCACCTTGTG | CTGCTCCCAAGAAAT | TTGTACCTTTTACTTGGAA | CATGAGCCCTCAGA | 720 |
| Qy | 721 | TTTTTAACTCT | AGTGTCAAAATTTT | AGGCCCAAAATATGATG | AGAAATATCTTAT | 780 |
| Db | 721 | TTTTTAACTCT | AGTGTCAAAATTTT | AGGCCCAAAATATGATG | AGAAATATCTTAT | 780 |
| Qy | 781 | TTCTTCAG | AAAAAATTGGAGAAAC | CTGCTGTCATCAAG | CTTTGACAGATGTGCATC | 840 |
| Db | 781 | TTCTTCAG | AAAAAATTGGAGAAAC | CTGCTGTCATCAAG | CTTTGACAGATGTGCATC | 840 |
| Qy | 841 | CAAGCTTTGAC | TCAAAA | CAAAATAGCCAGTATAT | TTCACTAAGTCAAAAT | 900 |
| Db | 841 | CAAGCTTTGAC | TCAAAA | CAAAATAGCCAGTATAT | TTCACTAAGTCAAAAT | 900 |
| Qy | 901 | CTTCAGAA | ATTGGATGCTAAGTATG | ATGACATPAAGTTAT | TCCACAGACAGCTCCAAAT | 960 |
| Db | 901 | CTTCAGAA | ATTGGATGCTAAGTATG | ATGACATPAAGTTAT | TCCACAGACAGCTCCAAAT | 960 |
| Qy | 961 | ATTTTCCCTCCG | CACTACTTGTACTAT | PACTAGTAATG | AGAGATGAATATGAGTTCAATC | 1020 |
| Db | 961 | ATTTTCCCTCCG | CACTACTTGTACTAT | PACTAGTAATG | AGAGATGAATATGAGTTCAATC | 1020 |
| Qy | 1021 | TTGTTGATG | TGCTGTTGCTACTG | TTCGTGATCCGGCGTTAT | TATTCATATGACGTTGCAA | 1080 |
| Db | 1021 | TTGTTGATG | TGCTGTTGCTACTG | TTCGTGATCCGGCGTTAT | TATTCATATGACGTTGCAA | 1080 |
| Qy | 1081 | CGAGACTTG | CAAAAGATCCAGAT | TTTGCTTCAATTAG | ATGATAGAG 1128 | |
| Db | 1081 | CGAGACTTG | CAAAAGATCCAGAT | TTTGCTTCAATTAG | ATGATAGAG 1128 | |

| RESULT 2 | AX193968 | 1128 bp | DNA | linear | PAT 15-AUG-2001 |
|------------|--|-------------|-----|--------|-----------------|
| LOCUS | AX193968 | | | | |
| DEFINITION | Sequence 246 from Patent WO0149834. | | | | |
| ACCESSION | AX193968 | | | | |
| VERSION | AX193968.1 | GI:15211580 | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | | | | | |
| REFERENCE | | | | | |
| AUTHORS | | | | | |
| TITLE | | | | | |
| JOURNAL | | | | | |
| | Albhai, M.F., Astwood, J.D., McWhetter, C.A. and Sampson, H.A. | | | | |
| | Preparation of deaerogenized proteins and permutins | | | | |
| | Patent: WO 0149834-A 246 12-JUL-2001; | | | | |
| | 1 | | | | |
| | other sequences; artificial sequences. | | | | |
| | synthetic construct | | | | |
| | synthetic construct | | | | |

| MONSANTO COMPANY (US) | | | |
|----------------------------|---------------------------------|-------------------|-------------------|
| FEATURES | Location/Qualifiers | | |
| source | 1. 1128 | | |
| | /organism="synthetic construct" | | |
| | /mol_type="unassigned DNA" | | |
| | /db_xref="taxon:32630" | | |
| | /note="Synthetic construct" | | |
| ORIGIN | | | |
| Query Match | 100.0% | Score 1128; DB 6; | Length 1128; |
| Best Local Similarity | 100.0%; | Prod. No. 1e-221; | |
| Matches 1128; Conservative | 0; Mismatches | 0; | Indels 0; Gaps 0; |

| | | | |
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| OY | 1 | TCGAGAAAAGAGAGGCTGGAAGCTTCATGTGAATTCAAAAAAATGCTGTGCTCTCATATAG | 60 |
| Db | 1 | TCGAGAAAAGAGAGGCTGGAAGCTTCATGTGAATTCAAAAAAATGCTGTGCTCTCATATAG | 60 |
| OY | 61 | GCACCTGGCACTACTTCAGAGCTTTGATATAAAATATATACGCAAAAAGAGCAGCTACTGGGA | 120 |
| Db | 61 | GCACCTGGCACTACTTCAGAGCTTTGATATAAAATATATACGCAAAAAGAGCAGCTACTGGGA | 120 |
| OY | 121 | CTGCTGTACATTTGGATGTTAGTTATATACGAAAAATGACTGATGCAAGAGTTCCTACATGA | 180 |
| Db | 121 | CTGCTGTACATTTGGATGTTAGTTATATACGAAAAATGACTGATGCAAGAGTTCCTACATGA | 180 |
| OY | 181 | CTGATTAATTACCTTTCTACTGCTCTTTCAAGCTCTGATTCAAAAACCAATTACTCAGGG | 240 |
| Db | 181 | CTGATTAATTACCTTTCTACTGCTCTTTCAAGCTCTGATTCAAAAACCAATTACTCAGGG | 240 |
| OY | 241 | TTCAAGAAAAATGCATTACAGGCAACACTACTGAAAATGGATGATGCTTCTGAGGCTATA | 300 |
| Db | 241 | TTCAAGAAAAATGCATTACAGGCAACACTACTGAAAATGGATGATGCTTCTGAGGCTATA | 300 |
| OY | 301 | TGGAATTATTAGTACAAAGTTGGTGAATACTTATTGAAGAAACCAAGTTTCGAGACAAATC | 360 |
| Db | 301 | TGGAATTATTAGTACAAAGTTGGTGAATACTTATTGAAGAAACCAAGTTTCGAGACAAATC | 360 |
| OY | 361 | CTGAACCTTATGAGGAAGCTCTATAAGAGTTTGCAAAATGCTCTGTGATGGAAGAAAC | 420 |
| Db | 361 | CTGAACCTTATGAGGAAGCTCTATAAGAGTTTGCAAAATGCTCTGTGATGGAAGAAAC | 420 |
| OY | 421 | TCCGAGCAAAACAAAGCTTCTTATGAGACAGAGCAAGTTGGGAGAAATGGTGACTTCTTA | 480 |
| Db | 421 | TCCGAGCAAAACAAAGCTTCTTATGAGACAGAGCAAGTTGGGAGAAATGGTGACTTCTTA | 480 |
| OY | 481 | GTAATTGATGAGAGTGAATTTAGAGGAATCATTTCCGGCTACCATTTCTGAAATTTCTTGAAG | 540 |
| Db | 481 | GTAATTGATGAGAGTGAATTTAGAGGAATCATTTCCGGCTACCATTTCTGAAATTTCTTGAAG | 540 |
| OY | 541 | GACAACTTCAGGGAATGGAACAAATATACAGATGCAAGCACTTGSCAGATTACTTGTATGTA | 600 |
| Db | 541 | GACAACTTCAGGGAATGGAACAAATATATGCAATGCAAGCACTTGSCAGATTACTTGTATGTA | 600 |
| OY | 601 | TTGGAGGAACAAGTACAGAGGTTTATTTGACTGCTATGATATAGTACTTCAAAATGAAAACA | 660 |
| Db | 601 | TTGGAGGAACAAGTACAGAGGTTTATTTGACTGCTATGATATAGTACTTCAAAATGAAAACA | 660 |
| OY | 661 | ATCGAACCTTTGCTGCTGCTGCCAABAAGATTTGTAACCTTTTACTTGGAACTAGGCCCTCAGA | 720 |
| Db | 661 | ATCGAACCTTTGCTGCTGCTGCCAABAAGATTTGTAACCTTTTACTTGGAACTAGGCCCTCAGA | 720 |
| OY | 721 | TTTTTAATCTAGTGGTCAAAATTTTATAGGCCCAAAATATGATGAGAAAAATATCTTATGCAAG | 780 |
| Db | 721 | TTTTTAATCTAGTGGTCAAAATTTTATAGGCCCAAAATATGATGAGAAAAATATCTTATGCAAG | 780 |
| OY | 781 | TTCTTCAAGAAAACTTGGAGAAACCTGCTGTGCAATCAAGCTTTGACAGAAAGTTGTCACT | 840 |
| Db | 781 | TTCTTCAAGAAAACTTGGAGAAACCTGCTGTGCAATCAAGCTTTGACAGAAAGTTGTCACT | 840 |
| OY | 841 | CAAGCTTTGACATCAAAACAAATTAAGCAGTAATTTCACTAAGTCAAAATTTAGCAAACT | 900 |
| Db | 841 | CAAGCTTTGACATCAAAACAAATTAAGCAGTAATTTCACTAAGTCAAAATTTAGCAAACT | 900 |

| | | | |
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| Qy | 901 | CTCCAGATTGGAGTGCCTAAGATGCTATGACATTAAGTATTTCACACGACAGCTCCAAAT | 960 |
| Db | 901 | CTCCAGATTGGAGTGCCTAAGATGCTATGACATTAAGTATTTCACACGACAGCTCCAAAT | 960 |
| Qy | 961 | ATTTTCCCTCCCATTAATCTTGTGTACTAATTAAGTAAAGAGATGAAATATGATTCATC | 1020 |
| Db | 961 | ATTTTCCCTCCCATTAATCTTGTGTACTAATTAAGTAAAGAGATGAAATATGATTCATC | 1020 |
| Qy | 1021 | TTGTGTATGATGCTGCTGCTAATCTGTTGCTGATCCGGCGTTATTTATCCATTAGCGTTGCA | 1080 |
| Db | 1021 | TTGTGTATGATGCTGCTGCTAATCTGTTGCTGATCCGGCGTTATTTATCCATTAGCGTTGCA | 1080 |
| Qy | 1081 | CGAAGCTTGCACAAAAGATCCAGATTTGCTCAATTAAGTAAGAG | 1128 |
| Db | 1081 | CGAAGCTTGCACAAAAGATCCAGATTTGCTCAATTAAGTAAGAG | 1128 |
| RESULT 3 | | | |
| LOCUS | AR412275 | 1128 bp | DNA |
| DEFINITION | Sequence 258 from patent US 6639054. | linear | PAT 18-DEC-2003 |
| ACCESSION | AR412275 | | |
| VERSION | AR412275.1 | GI:40167073 | |
| KEYWORDS | | | |
| SOURCE | unknown. | | |
| ORGANISM | unknown. | | |
| REFERENCE | 1 (bases 1 to 1128) | | |
| AUTHORS | Alibhai,M.F., Astwood,J.D., McWherter,C.A. and Sampson,H.A. | | |
| TITLE | Preparation of deaerogenized proteins and permutins | | |
| JOURNAL | Patent: US 6639054-A 258 28-OCT-2003; | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..1128 | | |
| ORIGIN | /organism="unknown" | | |
| | /mol_type="genomic DNA" | | |
| Query Match | 91.9%; | Score 1036.2; | DB 6; |
| Best Local Similarity | 99.2%; | Fred. No. 7.8e-203; | Length 1128; |
| Matches 1041; | Conservative | 0; | Mismatches 8; |
| | | Indels | 0; |
| | | Gaps | 0; |
| Qy | 77 | AGAGTTTATTAACATATACAGCAAAAGGACGACTACCTGACCTGTACATTGGAT | 136 |
| Db | 11 | AGAGGCTAGACTACATATACAGCAAAAGGACGACTACCTGACCTGTACATTGGAT | 70 |
| Qy | 137 | GTTAGTTATACAGAAATGACTGATGACGACAACTTCTACATGACTGATTTACCTTTC | 196 |
| Db | 71 | GTTAGTTATACAGAAATGACTGATGACGACAACTTCTACATGACTGATTTACCTTTC | 130 |
| Qy | 197 | TACTGCTTTCAAGCTCTTGATTTCAAAAAACAATTACTCAGGGTTCAAGAAATGCATT | 256 |
| Db | 131 | TACTGCTTTCAAGCTCTTGATTTCAAAAAACAATTACTCAGGGTTCAAGAAATGCATT | 190 |
| Qy | 257 | AACAGGCAACACTACTGAATGATGATGCTTCTGAGGCTAAATGAAATTAATAGTACA | 316 |
| Db | 191 | AACAGGCAACACTACTGAATGATGATGCTTCTGAGGCTAAATGAAATTAATAGTACA | 250 |
| Qy | 317 | AGTTGTGAATACTTATTTGAAAGAAACAAGTTTCGAGACAAATCTGAAACCTATGAGGA | 376 |
| Db | 251 | AGTTGTGAATACTTATTTGAAAGAAACAAGTTTCGAGACAAATCTGAAACCTATGAGGA | 310 |
| Qy | 377 | AGCTCTAAGAGTTTGGAAAATTTGCTCTGATGAGAAAGAACTCCGAGAAACCAAGC | 436 |
| Db | 311 | AGCTCTAAGAGTTTGGAAAATTTGCTCTGATGAGAAAGAACTCCGATCAACAAAGC | 370 |
| Qy | 437 | TTCTTATGACACAGACAGTTGGGAAATGTGACTGTTCTAGTATTTGATGAGAGTGG | 496 |
| Db | 371 | TTCTTATGACACAGACAGTTGGGAAATGTGACTGTTCTAGTATTTGATGAGAGTGG | 430 |
| Qy | 497 | AATTAGAGGATCATTTCCGGCTACCATTTCTGGAATTTCTTGAAGACAATTCAGAGAAAT | 556 |
| Db | 431 | AATTAGAGGATCATTTCCGGCTACCATTTCTGGAATTTCTTGAAGACAATTCAGAGAAAT | 490 |

| | | | | | |
|-----------------------|---|--|---------------|--------------|-----------------|
| Qy | 557 | GGACAAATATGCATGTGAAACCTTGAGATCTTTGATGTATTTGAGAAACAATGAC | 616 | | |
| Db | 491 | GGACAAATATGCATGTGAAACCTTGAGATCTTTGATGTATTTGAGAAACAATGAC | 550 | | |
| Qy | 617 | AGAGAGTTTATGACTGCTATGATTAAGTACTCCAAATGAAACATGACCCCTTGGCTGC | 676 | | |
| Db | 551 | AGAGAGTTTATGACTGCTATGATTAAGTACTCCAAATGAAACATGACCCCTTGGCTGC | 610 | | |
| Qy | 677 | TGCCAAGAAATTTGACCTTTTAACTTCGAAATGCGCCCTCAGATTTTAAATCTAGTGG | 736 | | |
| Db | 611 | TGCCAAGAAATTTGACCTTTTAACTTCGAAATGCGCCCTCAGATTTTAAATCTAGTGG | 670 | | |
| Qy | 737 | TCAATTTTAGAGCCCAAAATATGATGGAATAATCTTATGCAAGTTCTTCAGAAAAACT | 796 | | |
| Db | 671 | TCAATTTTAGAGCCCAAAATATGATGGAATAATCTTATGCAAGTTCTTCAGAAAAACT | 730 | | |
| Qy | 797 | TGGAAGAACTGCTGTGCATTCAGAGCTTTGACAGAGTTGTCACTTCAAGCTTTGACATCA | 856 | | |
| Db | 731 | TGGAAGAACTGCTGTGCATTCAGAGCTTTGACAGAGTTGTCACTTCAAGCTTTGACATCA | 790 | | |
| Qy | 857 | AACAAATTAAGCCAGTAATATTCACCTAAATGCAAACTCTCCAGATTTGATGTC | 916 | | |
| Db | 791 | AACAAATTAAGCCAGTAATATTCACCTAAATGCAAACTCTCCAGATTTGATGTC | 850 | | |
| Qy | 917 | TAAAGTATATACATTAAGTATTTCCACAGCAGCGCTCCAAATATTTTCTCCGCAATTA | 976 | | |
| Db | 851 | TAAAGTATATACATTAAGTATTTCCACAGCAGCGCTCCAAATATTTTCTCCGCAATTA | 910 | | |
| Qy | 977 | CTTTGTTATCTAATCTAGTAAATGAGATGAAATATGAGTTCAATCTTGTGATGGTGCCTG | 1036 | | |
| Db | 911 | CTTTGTTATCTAATCTAGTAAATGAGATGAAATATGAGTTCAATCTTGTGATGGTGCCTG | 970 | | |
| Qy | 1037 | TGCTACTGTTCCTATCCGCGGCTTATTTCCATTAGCGTTGCAACGAGACTTGCACAAA | 1096 | | |
| Db | 971 | TGCTACTGTTCCTATCCGCGGCTTATTTCCATTAGCGTTGCAACGAGACTTGCACAAA | 1030 | | |
| Qy | 1097 | GGATCCAGCATTTTGCTTCAATTAGGTAAT | 1125 | | |
| Db | 1031 | GGATCCAGCATTTTGCTTCAATTAGGTAAT | 1059 | | |
| RESULT 4 | AX193980 | 1128 bp | DNA | linear | PAT 15-AUG-2001 |
| LOCUS | AX193980 | | | | |
| DEFINITION | Sequence 258 from Patent WO0149834. | | | | |
| ACCESSION | AX193980 | | | | |
| VERSION | AX193980.1 | GI:15211589 | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | | | | | |
| REFERENCE | 1 | | | | |
| AUTHORS | Alibhai,M.F., Actwood,J.D., Mcwhorter,C.A. and Sampson,H.A. | | | | |
| TITLE | Preparation of deaerilegrentized proteins and permutelins | | | | |
| JOURNAL | Patent: WO 0149834-A 258 12-JUL-2001; | | | | |
| | MONSANTO COMPANY (US) | | | | |
| FEATURES | | | | | |
| source | | | | | |
| | location/Qualifiers | | | | |
| | 1..1128 | | | | |
| | /organism="synthetic construct" | | | | |
| | /mol_type="unassigned DNA" | | | | |
| | /db_xref="taxon:32630" | | | | |
| | /note="Synthetic construct" | | | | |
| ORIGIN | | | | | |
| Query Match | 91.9% | Score 1036.2; | DB 6; | Length 1128; | |
| Best Local Similarity | 99.2%; | Pred. No. 7.8e-203; | | | |
| Matches 1041; | Conservative | 0; | Mismatches 8; | Indels 0; | Gaps 0; |
| Qy | 77 | AGAGTTTATTAACATATACAGAGAAAGAGCGAGCTTACCTGACCTGCTGATCTTGAT | 136 | | |
| Db | 11 | AGAGGCTTAAGCTACATATACAGAGAAAGAGCGAGCTTACCTGACCTGCTGATCTTGAT | 70 | | |
| Qy | 137 | GTTAGTTATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATATTTATCACTTTC | 196 | | |

Db 71 GTTATGTTATACGAAATGACTGATGACAGAGTTCTTACATGATGATTTATACCTTTC 130
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Db 131 TACTGCTTTTCAAGCTCTTGATTCAAAACAAATTAACCTGAGGTTTCAAGAAATGCAAT 190
QY 257 AACAGGACACACTACTGAAATGATGATGCTTCTGAGGCTTAATATGGAATTTATTAGTACA 316
Db 191 AACAGGACACACTACTGAAATGATGATGCTTCTGAGGCTTAATATGGAATTTATTAGTACA 250
QY 317 AGTTGGTGAACCTTATTGAAAGAACCAAGTTTCCGAGACAAATCTGGAACCTATGAGA 376
Db 251 AGTTGGTGAACCTTATTGAAAGAACCAAGTTTCCGAGACAAATCTGGAACCTATGAGA 310
QY 377 AGCTTAAGAGGTTTGCAGAAATTTGCTCTCTGATAGGAGAAAATCCGAGCAAAAGC 436
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QY 497 AATTAGAGGATCAATTCGGCTACCAATTCGAAATTTCTGAAAGCAACTTGAGGAAT 556
Db 431 AATTAGAGGATCAATTCGGCTACCAATTCGAAATTTCTGAAAGCAACTTGAGGAAT 490
QY 557 GGAACAATATGACAGATGACAGACTTGACATTACTTTGATGATGATGAGGAACAAGTAC 616
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QY 917 TAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 976
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QY 977 CTCTTGTACTAATATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1036
Db 911 CTCTTGTACTAATATCTGATGATGATGATGATGATGATGATGATGATGATGATG 970
QY 1037 TGCTATCTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1096
Db 971 TGCTATCTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1030
QY 1097 GGATCCAGATTTGCTCAATTTAGTAAAT 1125
Db 1031 GGATCCAGATTTGCTCAATTTAGTAAAT 1059

RESULT 5
LOCUS AR412269 1128 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 250 from patent US 6639054.
ACCESSION AR412269

VERSION AR412269.1 GI:40167067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1128)
AUTHORS Alibhai, M.F., Astwood, J.D., McWhorter, C.A. and Sampson, H.A.
TITLE Preparation of deaerogenized proteins and permutins
JOURNAL Patent: US 6639054-A 250 28-Oct-2003;
FEATURES
source 1..1128
/organism="Unknown"
/mol_type="genomic DNA"
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Query Match 85.4%; Score 963.4; DB 6; Length 1128;
Best Local Similarity 99.9%; Pred. No. 7,3e-188;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTGATTAAGGCACTGGCACTTCAAGATT 83
Db 159 TCATTGAATTTACAAAAAATGCTGTTGCTCTGATTAAGGCACTGGCACTTCAAGATT 218
QY 84 GATTAACATATACAGCAAAAGAGGCACTGAGCTGCTGATGATGATGATGATGATGATG 143
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QY 144 ATACAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 203
Db 279 ATACAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 338
QY 204 TTTCAAGCTCTGATTTCAAAAAAATTAATCTCAGGCTTCAAGAAATGATTAACAGGC 263
Db 339 TTTCAAGCTCTGATTTCAAAAAAATTAATCTCAGGCTTCAAGAAATGATTAACAGGC 398
QY 264 ACAACTACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 323
Db 399 ACAACTACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 458
QY 324 GAAACCTTATGAAAGAACCAAGTTTCCAGAACCAATCTGAAACCTATGAGAAAGCTCTA 383
Db 459 GAAACCTTATGAAAGAACCAAGTTTCCAGAACCAATCTGAAACCTATGAGAAAGCTCTA 518
QY 384 AAGAGGTTTGAAGAAATTTGCTCTGATGATGATGATGATGATGATGATGATGATGATG 443
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Db 639 GGGATCAATTCGGCTACCAATTTCTGAAATTTCTGAAAGCAACTTCAGAAATGATG 698
QY 564 AATGCAATGCAAGCTTGCAATTTCTGATGATGATGATGATGATGATGATGATGATGATG 623
Db 699 AATGCAATGCAAGCTTGCAATTTCTGATGATGATGATGATGATGATGATGATGATGATG 758
QY 624 TTAATGACGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 683
Db 759 TTAATGACGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 818
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QY 744 TTAGGCCCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 803
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QY 804 ACTCGTGTGATCAAGCTTTGACAGAAATGATGATGATGATGATGATGATGATGATGATG 863

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Db 999 AAGCGATATATTTCAATGTAATTTTGGCAAACTCTCCAGATTTGATGCTAAGATG 1058
Qy 924 TATGACATTAAGTTATTTCCAGAGCAGCTTCAACATATTTTCTCCGCACTTACTTTGT 983
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Qy 984 ACTPA 988
Db 1119 ACTTA 1123

RESULT 6
AX193972 1128 bp DNA linear PAT 15-AUG-2001
LOCUS Sequence 250 from Patent WO0149834.
DEFINITION AX193972
ACCESSION AX193972
VERSION AX193972.1 GI:15211583
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Alibhai, M.F., Astwood, J.D., McWherter, C.A. and Sampson, H.A.
TITLE Preparation of deaerogenized proteins and permutins
JOURNAL Patent: WO 0149834-A 250 12-JUL-2001;
MONSANTO COMPANY (US)
FEATURES
source
1..1128
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic construct"

ORIGIN

Query Match 85.4%; Score 963.4; DB 6; Length 1128;
Best Local Similarity 99.9%; Pred. No. 7.3e-188;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 24 TCATTGATTTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTTACAGAGTTT 83
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Db 279 ATACAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 338
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Db 339 TTTCAGCTCTTATTTCAAAAAACAATTACCTGAGGCTTCAAGAAAATGCAATTAACAGGC 398
Qy 264 ACAACTACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323
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Qy 324 GAAAACTTATTTGAAGAAACAGGTTTCCGAAGACAACTCTGAAACCTTATGAGAAAGCTCTA 383
Db 459 GAAAACTTATTTGAAGAAACAGGTTTCCGAAGACAACTCTGAAACCTTATGAGAAAGCTCTA 518
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Db 519 AAGAGTTTCAAAATGCTCTCTGATAGGAAAGAACTCCGAGCAACCAAGCTTTCTTAT 578
Qy 444 GAGCCAGAGAGAGTTGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503
Db 579 GAGCCAGAGAGAGTTGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638

Qy 504 GGGATCATTCGGGCTACATTTCTGCAATTTCTTGAAGACAACCTTCAGAAATGCAAT 563
Db 639 GGGATCATTCGGGCTACATTTCTGCAATTTCTTGAAGACAACCTTCAGAAATGCAAT 698
Qy 564 AATGACATGCAAGACTTTCAGAGATTTACTTGTATGATGATGATGATGATGATGATGATGAT 623
Db 699 AATGACATGCAAGACTTTCAGAGATTTACTTGTATGATGATGATGATGATGATGATGATGAT 758
Qy 624 TTATGATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683
Db 759 TTATGATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
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Db 819 GAAATGTACCTTTTATTTTACCTGCAAGATGGCCCTCAGATTTTATTTTATCTTATGATGAT 878
Qy 744 TTAAGCCCAAAATATGATGAGAAATATCTTATGCAAGTTTCTTCAGAAAACTTGAAGAA 803
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Db 999 AAGCGATATATTTCAATGTAATTTTGGCAAACTCTCCAGATTTGATGCTAAGATG 1058
Qy 924 TATGACATTAAGTTATTTCCAGAGCAGCTTCAACATATTTTCTCCGCACTTACTTTGT 983
Db 1059 TATGACATTAAGTTATTTCCAGAGCAGCTTCAACATATTTTCTCCGCACTTACTTTGT 1118
Qy 984 ACTPA 988
Db 1119 ACTTA 1123

RESULT 7
AR412272 1128 bp DNA linear PAT 18-DEC-2003
LOCUS AR412272
DEFINITION Sequence 254 from patent US 6639054.
ACCESSION AR412272
VERSION AR412272.1 GI:40167070
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1128)
AUTHORS Alibhai, M.F., Astwood, J.D., McWherter, C.A. and Sampson, H.A.
TITLE Preparation of deaerogenized proteins and permutins
JOURNAL Patent: US 6639054-A 254 28-OCT-2003;
FEATURES
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/organism="unknown"
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ORIGIN

Query Match 80.6%; Score 909; DB 6; Length 1128;
Best Local Similarity 100.0%; Pred. No. 1.1e-176;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TCATTGATTTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTTACAGAGTTT 83
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Db 273 GATPAAAACATATACAGCAAAAGAGGAGCTAAGCTGGAATGCTGATGATGATGATGATGATGAT 332
Qy 144 ATACAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 203
Db 333 ATACAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 392

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QY 204 TTTCAGCTCTTGATTCAAAAAACAATTACCTCAGGGTTCAGAAAAATGCAATTAACAGGC 263
DB 393 TTTCAGCTCTTGATTCAAAAAACAATTACCTCAGGGTTCAGAAAAATGCAATTAACAGGC 452
QY 264 ACAACTACGTAAGTGAAGTGTCTGAGGCTAATATGGAATTTATAGTACAGTTGGT 323
DB 453 ACAACTACGTAAGTGAAGTGTCTGAGGCTAATATGGAATTTATAGTACAGTTGGT 512
QY 324 GAAATCTTATGGAAGAACAGTTTCCGAGACATCTGAAAACCTATGAGAGAGCTCTA 383
DB 513 GAAATCTTATGGAAGAACAGTTTCCGAGACATCTGAAAACCTATGAGAGAGCTCTA 572
QY 384 AAGAGTTTGCAAAATTTGCTCTGATGAGAGAACTCCGACAAACAAAGCTTTAT 443
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QY 444 GAGCCAGGACAGTTGGAGAAATGCTGCTCTTATGATGATGAGAGTGGAAATTAGA 503
DB 633 GAGCCAGGACAGTTGGAGAAATGCTGCTCTTATGATGATGAGAGTGGAAATTAGA 692
QY 504 GGGATCATTCGGGCTACCATTTCTGAAATTTCTTGAAGACACTTCAGAAATGACAAAT 563
DB 693 GGGATCATTCGGGCTACCATTTCTGAAATTTCTTGAAGACACTTCAGAAATGACAAAT 752
QY 564 AATGCAAGTCAAGACTTTCAGATTTCTTGAATGTAATTGAGAGAACAGTACAGAGT 623
DB 753 AATGCAAGTCAAGACTTTCAGATTTCTTGAATGTAATTGAGAGAACAGTACAGAGT 812
QY 624 TTATGACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683
DB 813 TTATGACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 872
QY 684 GAAATGTACCTTTTACTTGAACATGCGCTCAGATTTTATCTTATGCTGATGATGAT 743
DB 873 GAAATGTACCTTTTACTTGAACATGCGCTCAGATTTTATCTTATGCTGATGATGAT 932
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DB 933 TTAGGCCCCAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAACCTTGAAGAA 992
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DB 1053 AAGCCAGTATATTCCTAAGTCAAAATTTAGCAAACTCTCAGAAATGATGCTAAGATG 1112
QY 924 TATGACATA 932
DB 1113 TATGACATA 1121

RESULT 8
AX193976 1128 bp DNA linear PAT 15-AUG-2001
LOCUS Sequence 254 from Patent WO0149834.
DEFINITION AX193976
ACCESSION AX193976
VERSION AX193976.1 GI:15211586
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
OTHER SEQUENCES; artificial sequences.
REFERENCE
1 Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.
AUTHORS Preparation of deaerigenized proteins and permutins
TITLE Patent: WO 0149834-A 254 12-JUL-2001;
JOURNAL MONSANTO COMPANY (US)
FEATURES
location/Qualifiers
source 1..1128
/mol_type="synthetic construct"
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ORIGIN
Query Match 80.6%; Score 909; DB 6; Length 1128;
Best Local Similarity 100.0%; Pred. No. 1.1e-176;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/db_xref="taxon:32630"
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QY 24 TCATTAATTTACAAAAAATGCTGTGCTCTGATTAAGGCACTGCGACTTACAGGTT 83
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DB 273 GATAAAAACATTAACGCAAAAAAGAGAGCTTACCTGACCTGCTATATGATGATGAT 332
QY 144 ATACAGAAATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 203
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DB 453 ACAACTACGTAAGTGAAGTGTCTGAGGCTAATATGGAATTTATAGTACAGTTGGT 512
QY 324 GAAATCTTATGGAAGAACAGTTTCCGAGACATCTGAAAACCTATGAGAGAGCTCTA 383
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QY 384 AAGAGTTTGCAAAATTTGCTCTGATGAGAGAACTCCGACAAACAAAGCTTTAT 443
DB 573 AAGAGTTTGCAAAATTTGCTCTGATGAGAGAACTCCGACAAACAAAGCTTTAT 632
QY 444 GAGCCAGGACAGTTGGAGAAATGCTGCTCTTATGATGATGAGAGTGGAAATTAGA 503
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QY 504 GGGATCATTCGGGCTACCATTTCTGAAATTTCTTGAAGACACTTCAGAAATGACAAAT 563
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QY 564 AATGCAAGTCAAGACTTTCAGATTTCTTGAATGTAATTGAGAGAACAGTACAGAGT 623
DB 753 AATGCAAGTCAAGACTTTCAGATTTCTTGAATGTAATTGAGAGAACAGTACAGAGT 812
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DB 813 TTATGACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 872
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DB 1053 AAGCCAGTATATTCCTAAGTCAAAATTTAGCAAACTCTCAGAAATGATGCTAAGATG 1112
QY 924 TATGACATA 932
DB 1113 TATGACATA 1121

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RESULT 9
AR412278 1128 bp DNA linear PAT 18-DEC-2003
LOCUS AR412278
DEFINITION Sequence 262 from patent US 6639054.
ACCESSION AR412278
VERSION AR412278.1 GI:40167076
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1128)
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.
TITLE Preparation of deallergenized proteins and permutseins
JOURNAL Patent: US 6639054-A 262 28-OCT-2003;
FEATURES
source location/Qualifiers
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Query Match 77.9%; Score 879; DB 6; Length 1128;
Best Local Similarity 99.4%; Pred. No. 1.6e-170;
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 239 GGTTCAGAAAATGCACTTAACAGGCACTACTGAAATGATGCTTCTGAGGCTAA 238
DB 14 GGCTGAAGCTTAAGCTTTAAGGCACTACTGAAATGATGCTTCTGAGGCTAA 73
QY 299 TATGAATTTATTAAGTCAAGTTGGTGAATACTATTGMAAACAAGTTTCCGAGACA 358
DB 74 TATGAATTTATTAAGTCAAGTTGGTGAATACTATTGMAAACAAGTTTCCGAGACA 133
QY 359 TCCTGAACCTTATGAGAGAGCTCTAAAGAGTTTGCATAATTTGCTCTGATAGAGAA 418
DB 134 TCCTGAACCTTATGAGAGAGCTCTAAAGAGTTTGCATAATTTGCTCTGATAGAGAA 193
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DB 194 ACTCCGAGCAACAAAGCTCTTATGAGCAGAGCAGTTGGAGAAATGGGACTGTTCT 253
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DB 254 TAGTATTTGATGAGGTGATTAAGAGGATCAATTCGGGCTACCAATTCGAAATTTCTTGA 313
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DB 314 AGGACAACTTCAGAAATGAGCAATTAATGAGATGCAAGCTTCGAGATTACTTGATGT 373
QY 599 AATTGAGAGAACAAATGAGAGGTTTATGAGCTGATGATTAATGATGATGATGATGATG 658
DB 374 AATTGAGAGAACAAATGAGAGGTTTATGAGCTGATGATTAATGATGATGATGATGATG 433
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DB 434 CAATGACCTTTGCTGCTGCCAAAGAAATTTGATCCTTTTAACTTGCAGATGGCCCTCA 493
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DB 494 GATTTTAACTCTAGTGTCAAAATTTTAAAGCCCAAAATATGATGAAATATCTTATGCA 553
QY 779 AGTTTTCAGAAAATCTTGAGAAATCTGTCGATCAAGCTTTGACAGAAATTTGATGT 838
DB 554 AGTTTTCAGAAAATCTTGAGAAATCTGTCGATCAAGCTTTGACAGAAATTTGATGT 613
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QY 899 CTCCTCAGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
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DB 734 ATATTTTCCCGCATTAATTTGTTACTAATPACAGTAATGAGATGATGATGATGATGATGATG 793
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RESULT 10
AX193984 1128 bp DNA linear PAT 15-AUG-2001
LOCUS AX193984
DEFINITION Sequence 262 from Patent WO0149834.
ACCESSION AX193984
VERSION AX193984.1 GI:15211592
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.
TITLE Preparation of deallergenized proteins and permutseins
JOURNAL Patent: WO 0149834-A 262 12-JUL-2001;
MONSANTO COMPANY (US)
FEATURES
source location/Qualifiers
1..1128
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Query Match 77.9%; Score 879; DB 6; Length 1128;
Best Local Similarity 99.4%; Pred. No. 1.6e-170;
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 239 GGTTCAGAAAATGCACTTAACAGGCACTACTGAAATGATGCTTCTGAGGCTAA 238
DB 14 GGCTGAAGCTTAAGCTTTAAGGCACTACTGAAATGATGCTTCTGAGGCTAA 73
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DB 74 TATGAATTTATTAAGTCAAGTTGGTGAATACTATTGMAAACAAGTTTCCGAGACA 133
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QY 419 ACTCCGAGCAACAAAGCTCTTATGAGCAGAGCAGTTGGAGAAATGGGACTGTTCT 478
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DB 434 CAATGACCTTTGCTGCTGCCAAAGAAATTTGATCCTTTTAACTTGCAGATGGCCCTCA 493
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RESULT 11
AR412253 1138 bp DNA linear PAT 18-DEC-2003
LOCUS AR412253
DEFINITION Sequence 5 from patent US 6639054.
ACCESSION AR412253
VERSION AR412253.1 GI:40167051
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1138)
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.
TITLE Preparation of deaerogenized proteins and permutetins
JOURNAL Patent: US 6639054-A 5 28-OCT-2003;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 59.6%; Score 672.2; DB 6; Length 1138;
Best Local Similarity 99.6%; Pred. No. 5.5e-128;
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 449 AGGACAGTTGGAGAAATGCTGCTTTCTTATGATGATGAGAGTGAAGGAT 508
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Db 85 CATTCGGCTACCAATTCCTGAATTTCTTGAAGCAACTTCAGAAATGACAATATGC 144
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Db 685 TGCTTCAATTAAGTAAAT 701

RESULT 12
AX193727 1138 bp DNA linear PAT 15-AUG-2001
LOCUS AX193727
DEFINITION Sequence 5 from Patent WO0149834.
ACCESSION AX193727
VERSION AX193727.1 GI:15211567
KEYWORDS
SOURCE synthetic construct
ORGANISM Other sequences; artificial sequences.

REFERENCE 1
AUTHORS Alibhai,M.F., Astwood,J.D., McWhorter,C.A. and Sampson,H.A.
TITLE Preparation of deaerogenized proteins and permutetins
JOURNAL Patent: WO 0149834-A 5 12-JUL-2001;
FEATURES Location/Qualifiers
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/note="Synthetic construct"

ORIGIN

Query Match 59.6%; Score 672.2; DB 6; Length 1138;
Best Local Similarity 99.6%; Pred. No. 5.5e-128;
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 449 AGGACAGTTGGAGAAATGCTGCTTTCTTATGATGATGAGAGTGAAGGAT 508
Db 25 AGCTCAGTTGGAGAAATGCTGCTTTCTTATGATGATGAGAGTGAAGGAT 84
Qy 509 CATTCGGCTACCAATTCCTGAATTTCTTGAAGCAACTTCAGAAATGACAATATGC 568
Db 85 CATTCGGCTACCAATTCCTGAATTTCTTGAAGCAACTTCAGAAATGACAATATGC 144
Qy 569 AGATGCAAGCTTGCAATTAATTTGATGATGATGAGAAACAATGACAGAGTTATTT 628
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Db 685 TGCTCAATTAGGTAAT 701
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RESULT 13
AR412250 1158 bp DNA linear PAT 18-DEC-2003
LOCUS AR412250
DEFINITION Sequence 1 from patent US 6639054.
ACCESSION AR412250
VERSION AR412250.1 GI:40167048
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1158)
Alibhai, M.F., Astwood, J.D., McWhorter, C.A. and Sampson, H.A.
Preparation of deaerogenized proteins and permutins
Patent: US 6639054-A 1 28-OCT-2003;
Location/Qualifiers
1. 1158
/organism="unknown"
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ORIGIN

Query Match 59.5%; Score 671.4; DB 6; Length 1158;
Best Local Similarity 99.9%; Pred. No. 8e-128;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 453 CAGTTGGAGAAATGAGACTGTTCTTAGTATTGATGAGAGTGAATTAGAGGATCAT 512
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Db 70 CAGTTGGAGAAATGAGACTGTTCTTAGTATTGATGAGAGTGAATTAGAGGATCAT 129
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Db 130 CCGGCTACCAATTCGAAATTTCTTGAAGACAATTCAGAGAAATGACAATAATGCAGAT 189
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QY 573 GCAAGCTTGCAATTAATTTGATGATGAGAGAAACAATGAGAGATTTATGACT 632
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Db 190 GCAAGCTTGCAATTAATTTGATGATGAGAGAAACAATGAGAGATTTATGACT 249
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QY 633 GCTATGATAGTACTCCAAATGAAACAATGACCTTTGCTGCTGCAAGAAATTTGTA 692
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Db 250 GCTATGATAGTACTCCAAATGAAACAATGACCTTTGCTGCTGCAAGAAATTTGTA 309
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Db 490 ATATTCATTAAGTCAAAATTTAGCAACTCTCCAGAACTTGATGATGATGATGATGATGATGAT 549
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Db 730 TCAATTAGGTAAT 742
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RESULT 14
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LOCUS AX193723
DEFINITION Sequence 1 from Patent WO0149834.
ACCESSION AX193723
VERSION AX193723.1 GI:15211564
KEYWORDS
SOURCE
ORGANISM Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
1
Alibhai, M.F., Astwood, J.D., McWhorter, C.A. and Sampson, H.A.
Preparation of deaerogenized proteins and permutins
Patent: WO 0149834-A 1 12-JUL-2001;
MONSANTO COMPANY (US)
Location/Qualifiers
1. 1158
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ORIGIN

Query Match 59.5%; Score 671.4; DB 6; Length 1158;
Best Local Similarity 99.9%; Pred. No. 8e-128;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 453 CAGTTGGAGAAATGAGACTGTTCTTAGTATTGATGAGAGTGAATTAGAGGATCAT 512
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Db 70 CAGTTGGAGAAATGAGACTGTTCTTAGTATTGATGAGAGTGAATTAGAGGATCAT 129
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QY 633 GCTATGATAGTACTCCAAATGAAACAATGACCTTTGCTGCTGCAAGAAATTTGTA 692
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Db 730 TCAATTAGGTAAT 742
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QY 693 CTTTTTACTTGGACATGCGCCCTCAGATTTTAACTCAGTGTGCAAAATTTTAGGCCCA 752
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Db 310 CTTTTTACTTGGACATGCGCCCTCAGATTTTAACTCAGTGTGCAAAATTTTAGGCCCA 369
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QY 753 AAATATGATGGAATAATCTTATGCAAGTCTTCAAGAAAACCTGGAGAACTCGGTG 812
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Db 370 AAATATGATGGAATAATCTTATGCAAGTCTTCAAGAAAACCTGGAGAACTCGGTG 429
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QY 813 CATCAAGCTTGGACAGAAAGTGTCAATCTCAGCTTGGACATCAAAATTAAGCCAGTA 872
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Db 430 CATCAAGCTTGGACAGAAAGTGTCAATCTCAGCTTGGACATCAAAATTAAGCCAGTA 489
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QY 873 AATATCACTAAGTCAAAATTTAGCAAACTCTCCAGAAATGGATGCTAAGATGTAGACATA 932
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QY 1053 CCGGCGTTATTTATCCATTAGCGTTGCAAGAGACTTGCAAAAAGATCCAGCATTTGCT 1112
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Db 730 TCAATTAGGTAAT 742
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RESULT 15
AR412288 1161 bp DNA linear PAT 18-DEC-2003
LOCUS AR412288
DEFINITION Sequence 285 from patent US 6639054.
ACCESSION AR412288
VERSION AR412288.1 GI:40167086
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1161)
AUTHORS Alibhai M.F., Astwood J.D., McWhorter C.A. and Sampson H.A.
TITLE Preparation of deaerogenized proteins and permutetins
JOURNAL Patent: US 6639054-A 285 28-OCT-2003;
FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 8e-128;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 130 CCGGCTACATCTTCGAAATTTCTTGAAGACAACCTCAGAAAATGACAAATAATGAGAT 189
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QY 573 GCAAGACTTGCAATTAATTGATGTAATGAGAAACAAGTA CAGAGGTTTATTGACT 632
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QY 633 GCTATGATAGTACTCCAAATGAAAACAATGACCTTGTCTGTGCAAGAATAATTTGA 692
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Db 250 GCTATGATAGTACTCCAAATGAAAACAATGACCTTGTCTGTGCAAGAATAATTTGA 309
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 43 | 390.6 | 34.6 | 1164 | 2 | AAQ72603 | Aaq72603 Plant ins |
| 44 | 210.2 | 18.6 | 1506 | 6 | ABA01415 | Abao1415 Nicotiana |
| 45 | 185.6 | 16.5 | 1509 | 6 | ABA01417 | Abao1417 Nicotiana |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | AAH73832 standard; DNA; 1128 BP. |
| ID | AAH73832 |
| XX | AAH73832; |
| AC | AAH73832; |
| XX | 26-SEP-2001 (first entry) |
| DT | 26-SEP-2001 (first entry) |
| XX | Permuteln protein coding sequence #1. |
| DE | Permuteln protein coding sequence #1. |
| XX | Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity; |
| KW | larva growth; lipid acyl hydrolase; insecticide; ds. |
| KM | larva growth; lipid acyl hydrolase; insecticide; ds. |
| XX | Unidentified. |
| OS | Unidentified. |
| XX | Unidentified. |
| XX | WO200149834-A2. |
| PN | WO200149834-A2. |
| XX | 12-JUL-2001. |
| PD | 12-JUL-2001. |
| XX | 05-JAN-2001; 2001WO-US000342. |
| PF | 05-JAN-2001; 2001WO-US000342. |
| XX | 06-JAN-2000; 2000US-0174669P. |
| PR | 06-JAN-2000; 2000US-0174669P. |
| XX | (MONS) MONSANTO CO. |
| PA | (MONS) MONSANTO CO. |
| XX | Alibhai MF, Aetwood JD, McWherter CA, Sampson HA; |
| PI | Alibhai MF, Aetwood JD, McWherter CA, Sampson HA; |
| XX | WPI; 2001-441874/47. |
| DR | WPI; 2001-441874/47. |
| XX | Modified potato patatin proteins with reduced antigenicity, useful as |
| PT | insecticides for controlling e.g. round worm and root worm. |
| XX | insecticides for controlling e.g. round worm and root worm. |
| XX | Example 7, Page 182-183; 223pp; English. |
| PS | Example 7, Page 182-183; 223pp; English. |
| XX | The present invention relates to modified potato patatins that maintain |
| CC | enzymatic and insecticidal activity but which have reduced allergenicity. |
| CC | Groups (especially Tyr) which bind to anti-patatin antibodies were |
| CC | identified and glycosylation sites involved in antibody binding were |
| CC | removed via site directed mutagenesis. The patatins stunt the growth of |
| CC | larvae so that maturation is prevented or delayed. The patatins also have |
| CC | non-specific lipid acyl hydrolase activity. The modified patatins are |
| CC | also useful for inhibiting the activity of corn round worms. |
| CC | Deallergenised protein can be used as insecticides, as nutritional |

CC supplements and as immunising agents. The present sequence was used to
 CC illustrate the present invention
 XX
 SQ Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 1128; DB 4; Length 1128;
 Best Local Similarity 100.0%; Pred. No. 2.7e-291;
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TCAGAGAAAAGAGAGCTGAAGCTTCAATTGACAAAAAATGCTGCTCTCATTTAG 60
DB 1 TCAGAGAAAAGAGAGCTGAAGCTTCAATTGACAAAAAATGCTGCTCTCATTTAG 60
QY 61 GCACCTGGCACTACTTCAGAGTTGATTAACATATACAGAAAAGAGGACGTAACCTGA 120
DB 61 GCACCTGGCACTACTTCAGAGTTGATTAACATATACAGAAAAGAGGACGTAACCTGA 120
QY 121 CTGCTGTACATTTGATGATGATTAACAGAAAATGACTGATGACGAAAGTTTACATGA 180
DB 121 CTGCTGTACATTTGATGATGATTAACAGAAAATGACTGATGACGAAAGTTTACATGA 180
QY 181 CTGATATTACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAACAATTACCTCAGGG 240
DB 181 CTGATATTACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAACAATTACCTCAGGG 240
QY 241 TTCAGAAAAATGCAATTAACAGGCAACAATCTGAATGATGATGCTTCTGAGGCTTAAT 300
DB 241 TTCAGAAAAATGCAATTAACAGGCAACAATCTGAATGATGATGCTTCTGAGGCTTAAT 300
QY 301 TCGAATTTATATAGTACAAAGTTGATGAAAACTTATTTGAAGAAACGATTTCCGAAAGCAATC 360
DB 301 TCGAATTTATATAGTACAAAGTTGATGAAAACTTATTTGAAGAAACGATTTCCGAAAGCAATC 360
QY 361 CTGAAAACCTATGAGAAAGCTCTAAAGAGTTTGCAAAATGCTCTCTGATAGAGAAAC 420
DB 361 CTGAAAACCTATGAGAAAGCTCTAAAGAGTTTGCAAAATGCTCTCTGATAGAGAAAC 420
QY 421 TCCGAGCAAAACAAGCTTCTTATGACACAGACAGTTGGAGAAATGATGCTGTTCTTA 480
DB 421 TCCGAGCAAAACAAGCTTCTTATGACACAGACAGTTGGAGAAATGATGCTGTTCTTA 480
QY 481 GTATTGATGAGGTGAATTAAGAGGATCATTCGGCTACCAATTCGCAATTTCTTGAAG 540
DB 481 GTATTGATGAGGTGAATTAAGAGGATCATTCGGCTACCAATTCGCAATTTCTTGAAG 540
QY 541 GACAACCTTCAGAAATGAGCAATATATGCAATGCAAGATTCGAGATTACTTTGATGATTA 600
DB 541 GACAACCTTCAGAAATGAGCAATATATGCAATGCAAGATTCGAGATTACTTTGATGATTA 600
QY 601 TTGAGAGAACAGATACAGAGGTTTATGATGCTGATGATGATGATGATGATGATGATGAT 660
DB 601 TTGAGAGAACAGATACAGAGGTTTATGATGCTGATGATGATGATGATGATGATGATGAT 660
QY 661 ATGAGACCTTTGCTGCTGCCAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 ATGAGACCTTTGCTGCTGCCAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 TTTTATATCTAGTGTCAATTTATAGGCCCAAAATGATGATGATGATGATGATGATGATGAT 780
DB 721 TTTTATATCTAGTGTCAATTTATAGGCCCAAAATGATGATGATGATGATGATGATGATGAT 780
QY 781 TTTTCAAGAAAAAATGAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TTTTCAAGAAAAAATGAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 CAGGCTTGAATCAAAAAGAAATTAAGCAATATATGATGATGATGATGATGATGATGATGAT 900
DB 841 CAGGCTTGAATCAAAAAGAAATTAAGCAATATATGATGATGATGATGATGATGATGATGAT 900
QY 901 CTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 CTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

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QY 961 ATTTTCTCCGCAATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 961 ATTTTCTCCGCAATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
QY 1021 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 CGAGACTTGCACAAAAGATTCAGCAATTTGCTTCAATTAATGATGATGATGATGATGATGAT 1128
DB 1081 CGAGACTTGCACAAAAGATTCAGCAATTTGCTTCAATTAATGATGATGATGATGATGATGAT 1128

```

RESULT 2

```

ADM93059
ID ADM93059 standard; DNA; 1128 BP.
XX
AC ADM93059;
DT 03-JUN-2004 (first entry)
DE Permutated plasmid DNA #1.
XX
KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;
KW insect control; nutritional supplement; ds; permutated.
XX
OS Synthetic.
XX
PN US6657046-B1.
XX
PD 02-DEC-2003.
XX
PF 05-JAN-2001; 2001US-00755274.
XX
PR 06-JAN-2000; 2000US-0174669P.
PR 21-JUL-2000; 2000US-0219912P.
XX
PA (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI Alibhai MF, Rydel TJ;
XX
DR WPI; 2004-058368/06.
XX
DR P-PSDB; ADM93060.
XX
XX
XX New lipid acyl hydrolase proteins, useful for inhibiting insect
XX infestation of a plant or plant part, for controlling insects, as
XX nutritional supplements, or in immunotherapy protocols.
XX
XX Example 6; SEQ ID NO 20; 73pp; English.
XX
XX The invention relates to an isolated peptide exhibiting lipid acyl
XX hydrolase activity and corn rootworm insect inhibitory bioactivity. The
XX lipid acyl hydrolase peptide is useful for inhibiting insect infestation
XX of a plant or plant part, for controlling insects (e.g. corn rootworm),
XX as nutritional supplements, and in immunotherapy protocols. The present
XX sequence represents permutated plasmid DNA.
XX
SQ Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;
Query Match 100.0%; Score 1128; DB 12; Length 1128;
Best Local Similarity 100.0%; Pred. No. 2.7e-291;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAGAGAAAAGAGAGCTGAAGCTTCAATTGACAAAAAATGCTGCTCTCATTTAG 60
DB 1 TCAGAGAAAAGAGAGCTGAAGCTTCAATTGACAAAAAATGCTGCTCTCATTTAG 60
QY 61 GCACCTGGCACTACTTCAGAGTTGATTAACATATACAGAAAAGAGGACGTAACCTGA 120
DB 61 GCACCTGGCACTACTTCAGAGTTGATTAACATATACAGAAAAGAGGACGTAACCTGA 120
QY 121 CTGCTGTACATTTGATGATGATTAACAGAAAATGACTGATGACGAAAGTTTACATGA 180
DB 121 CTGCTGTACATTTGATGATGATTAACAGAAAATGACTGATGACGAAAGTTTACATGA 180

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| | | | |
|----|------|--|------|
| Db | 121 | CTGCTGTACATTTGGATGTTAGTATACGAAAAATGACATGACACCAAGTCTTACATGA | 180 |
| Qy | 181 | CTGATTTATTCACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTACCTCAGG | 240 |
| Db | 181 | CTGATTTATTCACCTTTCTACTGCTTTTCAAGCTCTTGATTCAAAAAACAATTACCTCAGG | 240 |
| Qy | 241 | TTTCAAGAAAAATGCACTTAAACAGGCACAATACTGAATATGATGCTTCTGAGGCTTAATA | 300 |
| Db | 241 | TTTCAAGAAAAATGCACTTAAACAGGCACAATACTGAATATGATGCTTCTGAGGCTTAATA | 300 |
| Qy | 301 | TGCAATTTATTTAGTCAAGTTGGTGAACAACTTATGAAAGAACCAAGTTTCCGAGACAATC | 360 |
| Db | 301 | TGCAATTTATTTAGTCAAGTTGGTGAACAACTTATGAAAGAACCAAGTTTCCGAGACAATC | 360 |
| Qy | 361 | CTGAACCTTATGAGAGAGCTCTAAAGAGTTTGCAAAATGTGCTCTGTATGAGAGAAAC | 420 |
| Db | 361 | CTGAACCTTATGAGAGAGAGCTCTAAAGAGTTTGCAAAATGTGCTCTGTATGAGAGAAAC | 420 |
| Qy | 421 | TTCCAGCAACAACAAAGCTCTTAATGACACAGACAGTGTGGAGAAATGATGACTGTCTTAA | 480 |
| Db | 421 | TTCCAGCAACAACAAGCTCTTAATGACACAGACAGTGTGGAGAAATGATGACTGTCTTAA | 480 |
| Qy | 481 | GTATTTGATGAGAGTGTGAATTTAGAGGATCATTCGCGCTACCAATTTCTGAAATTTCTTGAAG | 540 |
| Db | 481 | GTATTTGATGAGAGTGTGAATTTAGAGGATCATTCGCGCTACCAATTTCTGAAATTTCTTGAAG | 540 |
| Qy | 541 | GACAACTTCAGGAAATGAGCAATAATGACATGCAAGACTTGACAGATTACTTTGATGTDA | 600 |
| Db | 541 | GACAACTTCAGGAAATGAGCAATAATGACATGCAAGACTTGACAGATTACTTTGATGTDA | 600 |
| Qy | 601 | TTTGAAGAGAACAAATGACAGAGGTTTATGACCTGCTATGATAGTACTCCAAATGAAACA | 660 |
| Db | 601 | TTTGAAGAGAACAAATGACAGAGGTTTATGACCTGCTATGATAGTACTCCAAATGAAACA | 660 |
| Qy | 661 | ATGCACCTTTGCTGCTGCTCCAAAGAAATTTGATCCTTTTACTCGAAGATGGCCCTCAGA | 720 |
| Db | 661 | ATGCACCTTTGCTGCTGCTCCAAAGAAATTTGATCCTTTTACTCGAAGATGGCCCTCAGA | 720 |
| Qy | 721 | TTTTTTAATCTAGTGTGCAATTTTATGAGCCCAAAATATGATGAGAAATATCTTATGCAAG | 780 |
| Db | 721 | TTTTTTAATCTAGTGTGCAATTTTATGAGCCCAAAATATGATGAGAAATATCTTATGCAAG | 780 |
| Qy | 781 | TTCTTTCAAGAAAACTTGAAGAACTCGTGTGCATCAAGCTTTGACAGAAGTGTCACT | 840 |
| Db | 781 | TTCTTTCAAGAAAACTTGAAGAACTCGTGTGCATCAAGCTTTGACAGAAGTGTCACT | 840 |
| Qy | 841 | CAAGCTTTGACATCAAAAACAATAAGCAGTATATTTGACTAAGTCAAAATTTAGGAAACT | 900 |
| Db | 841 | CAAGCTTTGACATCAAAAACAATAAGCAGTATATTTGACTAAGTCAAAATTTAGGAAACT | 900 |
| Qy | 901 | CTCCAGAAATGAGATGCTAAGATGATGACATTAAGTTTCCACAGACAGCTCCAACT | 960 |
| Db | 901 | CTCCAGAAATGAGATGCTAAGATGATGACATTAAGTTTCCACAGACAGCTCCAACT | 960 |
| Qy | 961 | ATTTTTCCCTCCCATTACTTTGTTACTAATACTAAGTATGAGAAATGATGAGTCAATC | 1020 |
| Db | 961 | ATTTTTCCCTCCCATTACTTTGTTACTAATACTAAGTATGAGAAATGATGAGTCAATC | 1020 |
| Qy | 1021 | TTTGTGATGATGCTGTTGCTCTACTGTTGTGCTGATCCGCGCTTATTAATCAATTACGTTGCA | 1080 |
| Db | 1021 | TTTGTGATGATGCTGTTGCTCTACTGTTGTGCTGATCCGCGCTTATTAATCAATTACGTTGCA | 1080 |
| Qy | 1081 | CGAGACTTGACAAAAAGATCCAGCAATTTGCTTCAATTAAGTAAATGAG | 1128 |
| Db | 1081 | CGAGACTTGACAAAAAGATCCAGCAATTTGCTTCAATTAAGTAAATGAG | 1128 |

RESULT 3
AAH73841
ID AAH73841 standard; DNA; 1128 BP.
XX
AC AAH73841;
XX

| | | |
|----------------------------|---|---------------|
| DT | 28-SEP-2001 | (first entry) |
| DE | Permuterin protein coding sequence #4. | |
| KM | Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity; | |
| KW | larva growth; lipid acyl hydrolase; insecticide; ds. | |
| XX | | |
| OS | Unidentified. | |
| PN | MO200149834-A2. | |
| PD | 12-JUL-2001. | |
| PX | | |
| PF | 05-JAN-2001; 2001WO-US000342. | |
| PR | 06-JAN-2000; 2000US-0174669P. | |
| PA | (MONS) MONSANTO CO. | |
| PI | Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA; | |
| DR | WPI; 2001-441874/47. | |
| PT | Modified potato patatin proteins with reduced antigenicity, useful as | |
| PS | insecticides for controlling e.g. round worm and root worm. | |
| XX | | |
| XX | Example 10; Page 190; 223pp; English. | |
| CC | The present invention relates to modified potato patatins that maintain | |
| CC | enzymatic and insecticidal activity but which have reduced allergenicity. | |
| CC | Groups (especially Tyr) which bind to anti-patatin antibodies were | |
| CC | identified and glycosylation sites involved in antibody binding were | |
| CC | removed via site directed mutagenesis. The patatins stunt the growth of | |
| CC | larvae so that maturation is prevented or delayed. The patatins also have | |
| CC | non-specific lipid acyl hydrolase activity. The modified patatins are | |
| CC | also useful for inhibiting the activity of corn round worms. | |
| CC | Deaegerised protein can be used as insecticides, as nutritional | |
| CC | supplements and as immunising agents. The present sequence was used to | |
| CC | illustrate the present invention | |
| SQ | Sequence 1128 BP; 372 A; 202 C; 228 G; 326 T; 0 U; 0 Other; | |
| Query Match | 91.9%; Score 1036.2; DB 4; Length 1128; | |
| Best Local Similarity | 99.2%; Pred. No. 9.9e-267; | |
| Matches 1041; Conservative | 0; Mismatches 8; Indels 0; Gaps 0; | |
| DY | 77 AGAGTTTGATTAACCACTTATACGACAAGAAGCGACTTACCTGGACTGTGTACATTGGAT 136 | |
| DB | 11 AGAGGCTGAACCTCATATACAGCAAAAGAGCGACTTACCTGGACTGTGTACATTGGAT 70 | |
| DY | 137 GTTAGTTATACAGAAAATGACTGATGCGAAGTTCTTACATGACTGATTTTACCTTC 196 | |
| DB | 71 GTTAGTTATACAGAAAATGACTGATGCGAAGTTCTTACATGACTGATTTTACCTTC 130 | |
| DY | 197 TACTGCTTTTCAAGCTCTTGATTCAAAAAACATTAACCTCAGGGTTCAAGAAAATGCATT 256 | |
| DB | 131 TACTGCTTTTCAAGCTCTTGATTCAAAAAACATTAACCTCAGGGTTCAAGAAAATGCATT 190 | |
| DY | 257 AACAGGCCAACATCTACTGAATGATGATGCTTCTGAGGCTAATATGCAATTATTAATGACA 316 | |
| DB | 191 AACAGGCCAACATCTACTGAATGATGATGCTTCTGAGGCTAATATGCAATTATTAATGACA 250 | |
| DY | 317 AGTTGGTGAATACTTATGAGAAACAGCTTCCGAGAGCAATCCTGAAACCTATGAGGA 376 | |
| DB | 251 AGTTGGTGAATACTTATGAGAAACAGCTTCCGAGAGCAATCCTGAAACCTATGAGGA 310 | |
| DY | 377 AGCTCTAAGAAGTTTGGAAAATTCCTCTGATAGGAAGAACTCCGAGCAAACAAAGC 436 | |
| DB | 311 AGCTCTAAGAAGTTTGGAAAATTCCTCTGATAGGAAGAACTCCGATCAAACAAAGC 370 | |
| DY | 437 TTCTTATGACCAGGACAGTTGGGAGAAATGATGATCTTTTATGATATGAGAGGTGG 496 | |
| DB | 371 TTCTTATGACCAGGACAGTTGGGAGAAATGATGATCTTTTATGATATGAGAGGTGG 430 | |

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QY 497 AATTAGAGGATTCCTCCGCTACCAATTCCTGCAATTTCTTGAAGGACCACTTCAGGAAAT 556
DB 431 AATTAGAGGATTCCTCCGCTACCAATTCCTGCAATTTCTTGAAGGACCACTTCAGGAAAT 490
QY 557 GGCATTAATGAGCAGATGACAGACTTGAGATTAATCTTGAATTAATGAGGACCACTTCAGGAAAT 616
DB 491 GGCATTAATGAGCAGATGACAGACTTGAGATTAATCTTGAATTAATGAGGACCACTTCAGGAAAT 550
QY 617 AGGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAGCAATGCACTTTCGCTG 676
DB 551 AGGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAGCAATGCACTTTCGCTG 610
QY 677 TGCAGAAAGAAATGATCTTTTACTTTCGAAACATGCGCTCAGATTTTATCTTACTG 736
DB 611 TGCAGAAAGAAATGATCTTTTACTTTCGAAACATGCGCTCAGATTTTATCTTACTG 670
QY 737 TCAAAATTTAGGCGCCAAATATGATGAAATATCTTATGCAATTTCTTCAAAAAAAT 796
DB 671 TCAAAATTTAGGCGCCAAATATGATGAAATATCTTATGCAATTTCTTCAAAAAAAT 730
QY 797 TGGAGAACTCGTGTGATCAAGCTTTCAGAGAAATGTCATCTCAAGCTTTCAGATCAA 856
DB 731 TGGAGAACTCGTGTGATCAAGCTTTCAGAGAAATGTCATCTCAAGCTTTCAGATCAA 790
QY 857 AACCAATTAAGCCAGTATATTTCACTAAGTCAAAATTTAGCAAACTCTTCAGAAATTTGA 916
DB 791 AACCAATTAAGCCAGTATATTTCACTAAGTCAAAATTTAGCAAACTCTTCAGAAATTTGA 850
QY 917 TAAGATCTAGACATATGATTAATCCAGAGAGAGCTCCAAATTTCTTCGCAATTA 976
DB 851 TAAGATCTAGACATATGATTAATCCAGAGAGAGCTCCAAATTTCTTCGCAATTA 910
QY 977 CTCTGTTACTAATACTAGTATGAGATGAATATGAGTCAATCTTGTGATGAGTGT 1036
DB 911 CTCTGTTACTAATACTAGTATGAGATGAATATGAGTCAATCTTGTGATGAGTGT 970
QY 1037 TCGTACTGTTGCTGATCCGCGCTTATTAATCCATTAAGCTTTCAGAGCTTTCAGAA 1096
DB 971 TCGTACTGTTGCTGATCCGCGCTTATTAATCCATTAAGCTTTCAGAGCTTTCAGAA 1030
QY 1097 GGATCCAGATTTGCTTCAATTAAGTAT 1125
DB 1031 GGATCCAGATTTGCTTCAATTAAGTAT 1059

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RESULT 4

ADM93065 standard; DNA; 1128 BP.

ADM93065;

03-JUN-2004 (first entry)

Permutectin plasmid DNA #4.

lipid acyl hydrolase; corn rootworm; insect infestation; plant;

insect control; nutritional supplement; ds; permutectin.

Synthetic.

US6657046-B1.

02-DEC-2003.

05-JAN-2001; 2001US-00755274.

06-JAN-2000; 2000US-0174669P.

21-JUL-2000; 2000US-0219912P.

(MONS) MONSANTO TECHNOLOGY LLC.

Alibhai MF, Rydel TJ;

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XX MPI; 2004-058368/06.
DR P-PSDB; ADM93066.
XX
XX New lipid acyl hydrolase proteins, useful for inhibiting insect
PT infestation of a plant or plant part, for controlling insects, as
PT nutritional supplements, or in immunotherapy protocols.
XX
XX Example 6; SEQ ID NO 26; 73bp; English.
XX
XX The invention relates to an isolated peptide exhibiting lipid acyl
CC hydrolyse activity and corn rootworm insect inhibitory bioactivity. The
CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation
CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
CC as nutritional supplements, and in immunotherapy protocols. The present
CC sequence represents permutectin plasmid DNA.
XX
SQ Sequence 1128 BP; 372 A; 202 C; 228 G; 326 T; 0 U; 0 Other;

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Query Match 91.9%; Score 1036.2; DB 12; Length 1128;

Best Local Similarity 99.2%; Pred. No. 9.9e-267;

Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

QY 77 AGAGTTTGAATTAACATATACAGCAAGAGGAGCTACCTGAGCTGATGATGAT 136
DB 11 AGAGGCTGAAGCTACATATACAGCAAGAGGAGCTACCTGAGCTGATGATGAT 70
QY 137 GTTATGATTAACAGAAATGATGATGATGATGATGATGATGATGATGATGAT 196
DB 71 GTTATGATTAACAGAAATGATGATGATGATGATGATGATGATGATGATGAT 130
QY 197 TACTGCTTTTCAAGCTCTTGATTTCAAAAACATTAACCTCAGGCTTCAAGAAATGAT 256
DB 131 TACTGCTTTTCAAGCTCTTGATTTCAAAAACATTAACCTCAGGCTTCAAGAAATGAT 190
QY 257 AACAGCACAACACTAGCAATGATGATGATGATGATGATGATGATGATGATGAT 316
DB 191 AACAGCACAACACTAGCAATGATGATGATGATGATGATGATGATGATGATGAT 250
QY 317 AGTTGCTGAATTAATTAAGAAACAGTTTCCAGAGCAATCTCGAAACCTATGAGA 376
DB 251 AGTTGCTGAATTAATTAAGAAACAGTTTCCAGAGCAATCTCGAAACCTATGAGA 310
QY 377 AGCTCTAAAGAGGTTTGCAGAAATTTGCTCTGTATGAGAAAGAACTCCGAGCAAAAGC 436
DB 311 AGCTCTAAAGAGGTTTGCAGAAATTTGCTCTGTATGAGAAAGAACTCCGAGCAAAAGC 370
QY 437 TTCTTATGACCAAGGACAGTTGAGAGAAATGAGATGATGATGATGATGATGATGAT 496
DB 371 TTCTTATGACCAAGGACAGTTGAGAGAAATGAGATGATGATGATGATGATGATGAT 430
QY 497 AATTAGAGGATCAATCCGCGCTACATTCCTGCAATTTCTTGAAGGACCACTTCAGGAAAT 556
DB 431 AATTAGAGGATCAATCCGCGCTACATTCCTGCAATTTCTTGAAGGACCACTTCAGGAAAT 490
QY 557 GGCATTAATGAGCAGATGACAGACTTGAGATTAATCTTGAATTAATGAGGACCACTTCAGGAAAT 616
DB 491 GGCATTAATGAGCAGATGACAGACTTGAGATTAATCTTGAATTAATGAGGACCACTTCAGGAAAT 550
QY 617 AGGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAGCAATGCACTTTCGCTG 676
DB 551 AGGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAGCAATGCACTTTCGCTG 610
QY 677 TGCAGAAAGAAATGATCTTTTACTTTCGAAACATGCGCTCAGATTTTATCTTACTG 736
DB 611 TGCAGAAAGAAATGATCTTTTACTTTCGAAACATGCGCTCAGATTTTATCTTACTG 670
QY 737 TCAAAATTTAGGCGCCAAATATGATGAAATATCTTATGCAATTTCTTCAAAAAAAT 796
DB 671 TCAAAATTTAGGCGCCAAATATGATGAAATATCTTATGCAATTTCTTCAAAAAAAT 730
QY 797 TGGAGAACTCGTGTGATCAAGCTTTCAGAGAGAGCTTTCAGAGCTTTCAGATCAA 856

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ID ADM93061 standard; DNA; 1128 BP.
XX
AC ADM93061;
XX
DT 03-JUN-2004 (first entry)
XX
DE Permuterin plasmid DNA #2.
XX
KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;
insect control; nutritional supplement; ds; permuterin.
XX
OS Synthetic.
XX
PN US6657046-B1.
XX
PD 02-DEC-2003.
XX
PF 05-JAN-2001; 2001US-00755274.
XX
PR 06-JAN-2000; 2000US-0174669P.
XX
PR 21-JUL-2000; 2000US-0219912P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Alibhai MF, Rydel TJ;
XX
DR MPI; 2004-058368/06.
XX
DR P-PSDB; ADM93062.
XX
PT New lipid acyl hydrolase proteins, useful for inhibiting insect
infestation of a plant or plant part, for controlling insects, as
PT nutritional supplements, or in immunotherapy protocols.
XX
PS Example 6; SEQ ID NO 22; 73bp; English.
XX
CC The invention relates to an isolated peptide exhibiting lipid acyl
hydrolase activity and corn rootworm insect inhibitory bioactivity. The
CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation
of a plant or plant part, for controlling insects (e.g. corn rootworm),
CC as nutritional supplements, and in immunotherapy protocols. The present
CC sequence represents permuterin plasmid DNA.
XX
SQ Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 85.4%; Score 963.4; DB 12; Length 1128;
Best Local Similarity 99.9%; Pred. No. 3e-247;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 TCATTGAATTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTTTCAGAGTTT 83
DB 159 TCATTGAATTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTTTCAGAGTTT 218
QY 84 GATPAAACATATACAGCAAAAGAGGAGCTACCTGAGCTGCTGATCATTTAGTGT 143
DB 219 GATPAAACATATACAGCAAAAGAGGAGCTACCTGAGCTGCTGATCATTTAGTGT 278
QY 144 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTATTAACCTTCTACGCT 203
DB 279 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTATTAACCTTCTACGCT 338
QY 204 TTTCAGAGCTTTGATTCAAAAAACAATTAACCTGAGGGTTTGAAGAAATGATTAACAGGC 263
DB 339 TTTCAGAGCTTTGATTCAAAAAACAATTAACCTGAGGGTTTGAAGAAATGATTAACAGGC 398
QY 264 ACAAGTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTAATAGAACAGTTGGT 323
DB 399 ACAAGTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTAATAGAACAGTTGGT 458
QY 324 GAAAGCTTATTTGAAGAAACAGTTTCCGAGAGCAATCTGAAACCTATGAGAGCTCTA 383
DB 459 GAAAGCTTATTTGAAGAAACAGTTTCCGAGAGCAATCTGAAACCTATGAGAGCTCTA 518
QY 384 AAGAGGTTTGCAAAATTTGCTCTCTGATAGAGAAACTCCGAGCAAAACAAGCTTCTTAT 443

DB 519 AAGAGGTTTGCAAAATTTGCTCTCTGATAGAGAAACTCCGAGCAAAACAAGCTTCTTAT 578
QY 444 GAGCAGAGCAGTTGGAGAAATGATGACTGTTCTTATGATGATGAGAGTGAATTAAG 503
DB 579 GAGCAGAGCAGTTGGAGAAATGATGACTGTTCTTATGATGATGAGAGTGAATTAAG 638
QY 504 GGGATCATTCGGGCTACCAATTCGAAATTTCTTGAAGCAACTTCAGAAATGAGCAAT 563
DB 639 GGGATCATTCGGGCTACCAATTCGAAATTTCTTGAAGCAACTTCAGAAATGAGCAAT 698
QY 564 AATGAGATGCAAGACTTCGAGATTTCTTGAATTTGAGAGCAAGTACAGAGGT 623
DB 699 AATGAGATGCAAGACTTCGAGATTTCTTGAATTTGAGAGCAAGTACAGAGGT 758
QY 624 TTATTGACTGCTATGATTAAGTACTCCAAATGAAACCAATCGACCTTTCCTGTCGCAAA 683
DB 759 TTATTGACTGCTATGATTAAGTACTCCAAATGAAACCAATCGACCTTTCCTGTCGCAAA 818
QY 684 GAAATTTGACCTTTTACTTTCGAAACATGAGCCCTCAGATTTTATCTGATGCTCAAT 743
DB 819 GAAATTTGACCTTTTACTTTCGAAACATGAGCCCTCAGATTTTATCTGATGCTCAAT 878
QY 744 TTAGGCCCAAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAATCTTGAGAA 803
DB 879 TTAGGCCCAAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAATCTTGAGAA 938
QY 804 ACTGCTGATCATCAAGCTTTGACAGAGTTGCTATCTCAAGCTTTGACATCAAAACAAAT 863
DB 939 ACTGCTGATCATCAAGCTTTGACAGAGTTGCTATCTCAAGCTTTGACATCAAAACAAAT 998
QY 864 AAGCCGATATATTTCTGATGCAATTTTGAAGCAACTTCGAAATTTGATGCTAAGATG 923
DB 999 AAGCCGATATATTTCTGATGCAATTTTGAAGCAACTTCGAAATTTGATGCTAAGATG 1058
QY 924 TATGATATGATTTATTCACAGAGAGGCTCCAAATATTTCTCGGATTAATCTTGT 983
DB 1059 TATGATATGATTTATTCACAGAGAGGCTCCAAATATTTCTCGGATTAATCTTGT 1118
QY 984 ACTAA 988
DB 1119 ACTTA 1123

RESULT 7
AAH73838
ID AAH73838 standard; DNA; 1128 BP.
XX
AC AAH73838;
XX
DT 28-SEP-2001 (first entry)
XX
DE Permuterin protein coding sequence #3.
XX
KW Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
larva growth; lipid acyl hydrolase; insecticide; ds.
XX
OS Unidentified.
XX
PN W0200149834-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000342.
XX
PR 06-JAN-2000; 2000US-0174669P.
XX
PA (MONS) MONSANTO CO.
XX
PI Alibhai MF, Astwood JD, McWhorter CA, Sampson HA;
XX
DR MPI; 2001-441874/47.
XX

PT Modified potato patatin proteins with reduced antigenicity, useful as
 PT insecticides for controlling e.g. round worm and root worm.

PS Example 9; Page 187-188; 223pp; English.

XX The present invention relates to modified potato patatins that maintain
 CC enzymatic and insecticidal activity but which have reduced allergenicity.
 CC Groups (especially Tyr) which bind to anti-patatin antibodies were
 CC identified and glycosylation sites involved in antibody binding were
 CC removed via site directed mutagenesis. The patatins stunt the growth of
 CC larvae so that maturation is prevented or delayed. The patatins also have
 CC non-specific lipid acyl hydrolase activity. The modified patatins are
 CC also useful for inhibiting the activity of corn root worms.
 CC Deallergenised protein can be used as insecticides, as nutritional
 CC supplements and as immunising agents. The present sequence was used to
 CC illustrate the present invention

XX Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 80.6%; Score 909; DB 4; Length 1128;

Best Local Similarity 100.0%; Pred. No. 1.1e-232; Mismatches 0; Indels 0; Gaps 0;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TCATTGATTTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTTCAGAGTTT 83
 DB 213 TCATTGATTTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTTCAGAGTTT 272
 QY 84 GATPAAAACATATACAGCAAAAGGCGACGCTACCTGACCTGCTGACCTTGATTTAGTT 143
 DB 273 GATPAAAACATATACAGCAAAAGGCGACGCTACCTGACCTGCTGACCTTGATTTAGTT 332
 QY 144 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTACCTTCTTCTACTGCT 203
 DB 333 ATACAGAAATGACTGATGAGCAAGTTCTTACATGACTGATTTACCTTCTTCTACTGCT 392
 QY 204 TTTCAAGCTCTTATTCAAAAAACAATTAACCTCAGGCTTCAAGAAATGCAATTAACAGGC 263
 DB 393 TTTCAAGCTCTTATTCAAAAAACAATTAACCTCAGGCTTCAAGAAATGCAATTAACAGGC 452
 QY 264 ACAACTCTGAAATGATGATGCTTCTGAGGCTAATATGCAATTTATATGATCAAGTTGCT 323
 DB 453 ACAACTCTGAAATGATGATGCTTCTGAGGCTAATATGCAATTTATATGATCAAGTTGCT 512
 QY 324 GAAACCTTATGAGAAACAGGTTTCCGAGACCAATCCTGAAACCTTATGAGAGAGCTCTA 383
 DB 513 GAAACCTTATGAGAAACAGGTTTCCGAGACCAATCCTGAAACCTTATGAGAGAGCTCTA 572
 QY 384 AAGAGTTTGCAGAAATGCTCTCTGATGAGAAAGAACTCCGAGCAAAACAAGCTTCTTAT 443
 DB 573 AAGAGTTTGCAGAAATGCTCTCTGATGAGAAAGAACTCCGAGCAAAACAAGCTTCTTAT 632
 QY 444 GACACGAGCAGATGGGAGAAATGATGCTGTTCTTATGATTTATGAGAGTGGATTTAGA 503
 DB 633 GACACGAGCAGATGGGAGAAATGATGCTGTTCTTATGATTTATGAGAGTGGATTTAGA 692
 QY 504 GGGATCATTCGGGTATCAATTCCTGATTTCTGAAGCAAACTTCAGGAAATGGAACAT 563
 DB 693 GGGATCATTCGGGTATCAATTCCTGATTTCTGAAGCAAACTTCAGGAAATGGAACAT 752
 QY 564 AATGAGATGCAAGACTTGGAGATTTACTTGTATTTATGAGGAAACAAGTACAGAGGT 623
 DB 753 AATGAGATGCAAGACTTGGAGATTTACTTGTATTTATGAGGAAACAAGTACAGAGGT 812
 QY 624 TTAATGACTGCTATGATTAAGTACTCCAAATGAAAAACAATGACCTTGTCTGCTGCCAAA 683
 DB 813 TTAATGACTGCTATGATTAAGTACTCCAAATGAAAAACAATGACCTTGTCTGCTGCCAAA 872
 QY 684 GAAATGTACTTTTCTTCTGCAACATGGCCCTCAGATTTTATATCTAGAGTCAATTT 743
 DB 873 GAAATGTACTTTTCTTCTGCAACATGGCCCTCAGATTTTATATCTAGAGTCAATTT 932
 QY 744 TTAGGCCCAAAATATGATGAAAAATATCTATGCAAGTTCTTCAAGAAAACTTGGAGAA 803

DB 933 TTAGGCCCAAAATATGATGAAAAATATCTATGCAAGTTCTTCAAGAAAACTTGGAGAA 992
 QY 804 ACTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCTCAAGCTTTGACATCAAAACAAT 863
 DB 993 ACTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCTCAAGCTTTGACATCAAAACAAT 1052
 QY 864 AAGCAGTAATATTAATCACTTAAGTCAAAATTTAGCAAACTTCAGAAATTTGATGATG 923
 DB 1053 AAGCAGTAATATTAATCACTTAAGTCAAAATTTAGCAAACTTCAGAAATTTGATGATG 1112
 QY 924 TATGACATA 932
 DB 1113 TATGACATA 1121

RESULT 8

ADM93063 standard; DNA; 1128 BP.

AC ADM93063;

DT 03-JUN-2004 (first entry)

DE Permuterin plasmid DNA #3.

KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;

KW insect control; nutritional supplement; ds; permuterin.

OS Synthetic.

PN US6657046-B1.

PD 02-DEC-2003.

PF 05-JAN-2001; 2001US-00755274.

PR 06-JAN-2000; 2000US-0174669P.

PR 21-JUL-2000; 2000US-0219912P.

PA (MONS) MONSANTO TECHNOLOGY LLC.

PI Ailbhal MF, Rydel TJ;

DR WPI: 2004-058368/06.

DR P-PSDB; ADM93064.

PS New lipid acyl hydrolase proteins, useful for inhibiting insect

PT infestation of a plant or plant part, for controlling insects, as

PT nutritional supplements, or in immunotherapy protocols.

CC Example 6; SEQ ID NO 24; 73pp; English.

CC The invention relates to an isolated peptide exhibiting lipid acyl

CC hydrolyase activity and corn rootworm insect inhibitory bioactivity. The

CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),

CC as nutritional supplements, and in immunotherapy protocols. The present

CC sequence represents permuterin plasmid DNA.

XX Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;

Query Match 80.6%; Score 909; DB 12; Length 1128;

Best Local Similarity 100.0%; Pred. No. 1.1e-232; Mismatches 0; Indels 0; Gaps 0;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TCATTGATTTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTTCAGAGTTT 83

DB 213 TCATTGATTTACAAAAAATGCTGCTCTCATTTAGGCACTGGCACTACTTTCAGAGTTT 272

QY 84 GATPAAAACATATACAGCAAAAGGCGACGCTACCTGACCTGCTGACCTTGATTTAGTT 143

DB 273 GATPAAAACATATACAGCAAAAGGCGACGCTACCTGACCTGCTGACCTTGATTTAGTT 332

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QY 144 ATACAGAAATGACTGATGACGAAAGTTCTTACATGATGATTTACCTTTCTACTGCT 203
DB 333 ATACAGAAATGACTGATGACGAAAGTTCTTACATGATGATTTACCTTTCTACTGCT 392
QY 204 TTTCAGAGCTTGTATTCAAAAAACAATTTACTCAGGGTTCAAGAAATGATTAACAGGC 263
DB 393 TTTCAGAGCTTGTATTCAAAAAACAATTTACTCAGGGTTCAAGAAATGATTAACAGGC 452
QY 264 ACAACTACTGAAATGATGATGCTTCTGAGGCTTAATATGAAATTAATTAATGACAAAGTGGT 323
DB 453 ACAACTACTGAAATGATGATGCTTCTGAGGCTTAATATGAAATTAATTAATGACAAAGTGGT 512
QY 324 GAAACTTATTAAGAAACCAAGTTTCCGAAAGCAATCTGAAACCTTAATGAGAACTCTA 383
DB 513 GAAACTTATTAAGAAACCAAGTTTCCGAAAGCAATCTGAAACCTTAATGAGAACTCTA 572
QY 384 AAGAGGTTTGCAAAATGCTCTGATAGAGAACTCCGACCAACCAAGGTTCTTAT 443
DB 573 AAGAGGTTTGCAAAATGCTCTGATAGAGAACTCCGACCAACCAAGGTTCTTAT 632
QY 444 GACACGACAGTTGGAGAAATGATGATGCTTCTTATTAATGATGAGAGGTTGAAATTA 503
DB 633 GACACGACAGTTGGAGAAATGATGATGCTTCTTATTAATGATGAGAGGTTGAAATTA 692
QY 504 GGGATCATTCGGCTACCATTCGAAATTTCTTGAAGGACAACTTCAGAAATGACAAAT 563
DB 693 GGGATCATTCGGCTACCATTCGAAATTTCTTGAAGGACAACTTCAGAAATGACAAAT 752
QY 564 AATGACAGTCAAGACTGACAACTTCTTATGATGATTAATGAGAGAACTTACAGAGGT 623
DB 753 AATGACAGTCAAGACTGACAACTTCTTATGATGATTAATGAGAGAACTTACAGAGGT 812
QY 624 TTATGACTGCTATGATTAAGTACTCCAAATGAAACCAATGACCTTGTCTGCTCCAA 683
DB 813 TTATGACTGCTATGATTAAGTACTCCAAATGAAACCAATGACCTTGTCTGCTCCAA 872
QY 684 GAAATGATGCTTTTACTTGAACATGCGCTTCAGATTTTAACTTAACTGATGCTCAAT 743
DB 873 GAAATGATGCTTTTACTTGAACATGCGCTTCAGATTTTAACTTAACTGATGCTCAAT 932
QY 744 TTAGGCCCCAAATATGATGAGAAATATCTATGCAAGTCTTCAAGAAACCAATGAGAA 803
DB 933 TTAGGCCCCAAATATGATGAGAAATATCTATGCAAGTCTTCAAGAAACCAATGAGAA 992
QY 804 ACTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
DB 993 ACTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
QY 864 AAGCCAGTAATATCTAATGCAATTAATGCAAACTTCCAGAAATGATGATGATGATG 923
DB 1053 AAGCCAGTAATATCTAATGCAATTAATGCAAACTTCCAGAAATGATGATGATGATG 1112
QY 924 TATGACATA 932
DB 1113 TATGACATA 1121
```

RESULT 9
AAH73844
AAH73844 standard; DNA; 1128 BP.

AC AAH73844;

DT 28-SEP-2001 (first entry)

DE Permutate protein coding sequence #5.

KW Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;

KM larva growth; lipid acyl hydrolase; insecticide; ds.

OS Unidentified.

PN WO200149834-A2.

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XX 12-UTL-2001.
PD 05-JAN-2001; 2001WO-US000342.
PF 06-JAN-2000; 2000US-0174669P.
PR (MONS ) MONSANTO CO.
PA Alibhai MF, Actwood JD, Mcwherter CA, Sampson HA;
PI WPI; 2001-441874/47.
PT Modified potato patatin proteins with reduced antigenicity, useful as
PT insecticides for controlling e.g. round worm and root worm.
XX Example 11; Page 192-193; 223pp; English.
PS The present invention relates to modified potato patatins that maintain
CC enzymatic and insecticidal activity but which have reduced allergenicity.
CC Groups (especially Tyr) which bind to anti-patatin antibodies were
CC identified and glycosylation sites involved in antibody binding were
CC removed via site directed mutagenesis. The patatins stunt the growth of
CC larvae so that maturation is prevented or delayed. The patatins also have
CC non-specific lipid acyl hydrolase activity. The modified patatins are
CC also useful for inhibiting the activity of corn round worms.
CC Deallergens protein can be used as insecticides, as nutritional
CC supplements and as immunising agents. The present sequence was used to
CC illustrate the present invention
SQ Sequence 1128 BP; 372 A; 202 C; 229 G; 325 T; 0 U; 0 Other;
Query Match 77.9%; Score 879; DB 4; Length 1128;
Best Local Similarity 99.4%; Pred. No. 1.2e-224;
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 239 GGTTCAGAAATGCTTATTAACAGGCACTACTGAAATGATGATGCTTGAAGCTTA 298
DB 14 GGCTGAAGTAAATGCTTAAACAGGCACTACTGAAATGATGATGCTTGAAGCTTA 73
QY 299 TATGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 358
DB 74 TATGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 133
QY 359 TCCTGAAACCTATGAGAAAGCTCTAAAGAGTTTGAATTTGCTCTGATAGAA 418
DB 134 TCCTGAAACCTATGAGAAAGCTCTAAAGAGTTTGAATTTGCTCTGATAGAA 193
QY 419 ACTCGAGCAACAAAGCTTTTATGACACGAGCACTTGGAGAAATGATGATGATGAT 478
DB 194 ACTCGAGCAACAAAGCTTTTATGACACGAGCACTTGGAGAAATGATGATGATGATG 253
QY 479 TGTATGATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 538
DB 254 TGTATGATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 313
QY 539 AGGACAACTTCAAGAAATGAGCAATATGCAATGCAAGCTTCAATTTACTTTGATGT 598
DB 314 AGGACAACTTCAAGAAATGAGCAATATGCAATGCAAGCTTCAATTTACTTTGATGT 373
QY 599 AATTGAGAGCAACAGTACGAGGTTTATGATGATGATGATGATGATGATGATGATG 658
DB 374 AATTGAGAGCAACAGTACGAGGTTTATGATGATGATGATGATGATGATGATGATG 433
QY 659 CAATGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
DB 434 CAATGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 493
QY 719 GATTTTAAATCTAGTGTCAATTTTATGAGCCCAAAATATGATGAAATATCTTATGCA 778
DB 494 GATTTTAAATCTAGTGTCAATTTTATGAGCCCAAAATATGATGAAATATCTTATGCA 553
QY 779 AGTTCTTCAAGAAACCTTGAAGAACTGCTGTGATCAAGCTTTGACAGAACTGTCTAT 838
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| | | | |
|----|------|---|------|
| Db | 554 | AGTCTTAAAGAAAACCTTGGAGAACTCGTGCATCAAGCTTTGACAGAGTTGTAT | 613 |
| Qy | 839 | CTCAAGCTTTGACATCAAAACAAATAGCCAGTAATATTTACTAAGTCAAAATTTAGCAA | 898 |
| Db | 614 | CTCAAGCTTTGACATCAAAACAAATAGCCAGTAATATTTACTAAGTCAAAATTTAGCAA | 673 |
| Qy | 899 | CTCTCCAAATTTGATGCTAAGATGTATGACATTAAGTTATTTCCACAGCAGCGCTTCAAC | 958 |
| Db | 674 | CTCTCCAAATTTGATGCTAAGATGTATGACATTAAGTTATTTCCACAGCAGCGCTTCAAC | 733 |
| Qy | 959 | ATATTTTGCTCCGACTTACTTTGTACTAAATACATGATATGAGATGAAATATGATTCAA | 1011 |
| Db | 734 | ATATTTTGCTCCGACTTACTTTGTACTAAATACATGATATGAGATGAAATATGATTCAA | 793 |
| Qy | 1019 | TCTTGTTGATGATGCTGTGTGCTACTGTTGCTGATCCGCGGTTATTATCCATTAGCGTTGC | 1076 |
| Db | 794 | TCTTGTTGATGATGCTGTGTGCTACTGTTGCTGATCCGCGGTTATTATCCATTAGCGTTGC | 853 |
| Qy | 1079 | AACGAGATTCGACAAAGATCCGAGCTTTGCTTCATTATGAGTAAT | 1125 |
| Db | 854 | AACGAGATTCGACAAAGATCCGAGCTTTGCTTCATTATGAGTAAT | 900 |

| | | | |
|----|------|---|------|
| QY | 229 | GGTTCAAGAAAATGCATTAAACAGGACACAATACTGAATAATGATGATGCTTCTGAGGCTTAA | 298 |
| Db | 14 | GGCTGAACCTATATGCAATTAAACAGGACACAATACTGAATAATGATGATGCTTCTGAGGCTTAA | 73 |
| QY | 299 | TATGAAATTATTAATGACAAAGTTGGTGAAGAACTTATTTGAAGAAACAGTTTCCGAAGACAA | 358 |
| Db | 74 | TATGAAATTATTAATGACAAAGTTGGTGAAGAACTTATTTGAAGAAACAGTTTCCGAAGACAA | 133 |
| QY | 359 | TCTGGAACCTATGAGGAAGGCTTAAAGAGTTTGGCAAAATTGCTCTGTATGGAAGAA | 418 |
| Db | 134 | TCTGGAACCTATGAGGAAGGCTTAAAGAGTTTGGCAAAATTGCTCTGTATGGAAGAA | 193 |
| QY | 419 | ACTCCGAGCAACAAAGCTTCTTATGACACGAGACAGTTGGGAGAAATGCTGATCTTCT | 478 |
| Db | 194 | ACTCCGAGCAACAAAGCTTCTTATGACACGAGACAGTTGGGAGAAATGCTGATCTTCT | 253 |
| QY | 479 | TAGTATGATGAGAGTGAATTTAGAGGATCAATTCGGCTACACTTCGAAATTTCTTGA | 538 |
| Db | 254 | TAGTATGATGAGAGTGAATTTAGAGGATCAATTCGGCTACACTTCGAAATTTCTTGA | 313 |
| QY | 539 | AGGACAACTTGAGGAAATGACAAATAATGACAGATGCAAGACTTGCAGATTACTTTGATGT | 598 |
| Db | 314 | AGGACAACTTGAGGAAATGACAAATAATGACAGATGCAAGACTTGCAGATTACTTTGATGT | 373 |
| QY | 599 | AATTTGAGGAAACAAGTACAGAGGTTTATGACCTGATATGATTAAGTACTCCAAATGAAAA | 658 |
| Db | 374 | AATTTGAGGAAACAAGTACAGAGGTTTATGACCTGATATGATTAAGTACTCCAAATGAAAA | 433 |
| QY | 659 | CAATGACACCTTGTGCTGCCAAAGAAATTGTAACCTTTTATCTCGAACAATGGCCCTCA | 718 |
| Db | 434 | CAATGACACCTTGTGCTGCCAAAGAAATTGTAACCTTTTATCTCGAACAATGGCCCTCA | 493 |
| QY | 719 | GATTTTATCTTATGCTGCTCAAAATTTTATGGCCCAAAATATGATGGAATAATCTTATGCA | 778 |
| Db | 494 | GATTTTATCTTATGCTGCTCAAAATTTTATGGCCCAAAATATGATGGAATAATCTTATGCA | 553 |
| QY | 779 | AGTTCCTCAAGAAAACTTGGAGAAACTGTGTGATCAAGCTTTGACAGAAATTGTGAT | 838 |
| Db | 554 | AGTTCCTCAAGAAAACTTGGAGAAACTGTGTGATCAAGCTTTGACAGAAATTGTGAT | 613 |
| QY | 839 | CTCAAGCTTTGACATCAAAACAATTAAGCCAGTAAATTTCACATAAGTCAAAATTTAGCAAA | 898 |
| Db | 614 | CTCAAGCTTTGACATCAAAACAATTAAGCCAGTAAATTTCACATAAGTCAAAATTTAGCAAA | 673 |
| QY | 899 | CTTCCCAAAATTTGATGCTAGTAGATGATGACATTAAGTAAATTCACAGAGACGCTCCAAC | 958 |
| Db | 674 | CTTCCCAAAATTTGATGCTAGTAGATGATGACATTAAGTAAATTCACAGAGACGCTCCAAC | 733 |
| QY | 959 | ATATTTTCTCCGACTTACTTTGTTACTAATACTAGTATATGAGATGATAATGACTTCAA | 1018 |
| Db | 734 | ATATTTTCTCCGACTTACTTTGTTACTAATACTAGTATATGAGATGATAATGACTTCAA | 793 |
| QY | 1019 | TCTTGTGATGATGCTGTGTTGCTACTGTTGCTGATCCGGCGTTATTTATCCATTAGCGTTGC | 1078 |
| Db | 794 | TCTTGTGATGATGCTGTGTTGCTACTGTTGCTGATCCGGCGTTATTTATCCATTAGCGTTGC | 853 |
| QY | 1079 | AACGAGACTTGACAAAGAGATCCAGACTTTGCTTCAATTAGGTTAT | 1125 |
| Db | 854 | AACGAGACTTGACAAAGAGATCCAGACTTTGCTTCAATTAGGTTAT | 900 |

KW allergenicity; larva growth; lipid acyl hydrolase; insecticide; ss.
XX Synthetic.
XX MO200149834-A2.
XX
XX 12-JUL-2001.
XX
XX 05-JAN-2001; 2001MO-US000342.
XX
XX 06-JAN-2000; 2000US-0174669P.
XX
XX (MONS) MONSANTO CO.
XX
XX Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA;
XX
XX MPI; 2001-441874/47.
XX
XX Modified potato patatin proteins with reduced antigenicity, useful as
XX insecticides for controlling e.g. round worm and root worm.
XX
XX Example 5; Page 135-136; 223pp; English.
XX
XX The present invention relates to modified potato patatins that maintain
XX enzymatic and insecticidal activity but which have reduced allergenicity.
XX Groups (especially Tyr) which bind to anti-patatin antibodies were
XX identified and glycosylation sites involved in antibody binding were
XX removed via site directed mutagenesis. The patatins stunt the growth of
XX larvae so that maturation is prevented or delayed. The patatins also have
XX non-specific lipid acyl hydrolase activity. The modified patatins are
XX also useful for inhibiting the activity of corn round worms.
XX Deallergenised protein can be used as insecticides, as nutritional
XX supplements and as immunising agents. The present sequence is a PCR
XX primer, which was used in an example from the present invention
XX
XX Sequence 1138 BP; 374 A; 206 C; 229 G; 329 T; 0 U; 0 Other;
SQ
Query Match 59.6%; Score 672.2; DB 4; Length 1138;
Best Local Similarity 99.6%; Pred. No. 2.6e-169;
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 449 AGGACATTTGGGAGAAATGGTGACTGTTCTTAGATTGAGAGGATTTAGAGGAT 508
DB 25 AGCTCAGTTGGGAAATGGTGAAGTCTGTTCTTAGATTGAGAGGATTTAGAGGAT 84
QY 509 CATTCGGCTACCATCTCTCGAATTTCTTGAAGACAATTGAGAAATGACATATATGC 568
DB 85 CATTCGGCTACCATCTCTCGAATTTCTTGAAGACAATTGAGAAATGACATATATGC 144
QY 569 AGATGCAAGCTTGCAGATTACTTTGATGTAATTGAGAAACAATGAGAGGTTTATT 628
DB 145 AGATGCAAGCTTGCAGATTACTTTGATGTAATTGAGAAACAATGAGAGGTTTATT 204
QY 629 GATCGCATGATAGTACTGCAATGAAACATTCGACCTTTGCTGCTGCCAAGAAAT 688
DB 205 GATCGCATGATAGTACTGCAATGAAACATTCGACCTTTGCTGCTGCCAAGAAAT 264
QY 689 TGTAACCTTTTACTTGGACATGAGCCCTCGATTTTAAATCTTAAGTGTCAAAATTTAGG 748
DB 265 TGTAACCTTTTACTTGGACATGAGCCCTCGATTTTAAATCTTAAGTGTCAAAATTTAGG 324
QY 749 CCCAAATATGATGAAATATATCTTATGCAAGTTCTTCAAGAAATTTGAGAAATCTCG 808
DB 325 CCCAAATATGATGAAATATATCTTATGCAAGTTCTTCAAGAAATTTGAGAAATCTCG 384
QY 809 TGTCGATCAAGCTTGGACAGAGTGTCAATCTCAAGTTGATGATCAAAACAATTAAGCC 868
DB 385 TGTCGATCAAGCTTGGACAGAGTGTCAATCTCAAGTTGATGATCAAAACAATTAAGCC 444
QY 869 AGTAATATTCATTAAGTCAAAATTTAGCAAACTCTCCGAATTTGAGATGCTAAGATGTATGA 928
DB 445 AGTAATATTCATTAAGTCAAAATTTAGCAAACTCTCCGAATTTGAGATGCTAAGATGTATGA 504

QY 929 CATTAAGTTATTCACAGCAGAGCTCCACATATTTTCCCGCATTTACTTGTACTAA 988
DB 505 CATTAAGTTATTCACAGCAGAGCTCCACATATTTTCCCGCATTTACTTGTACTAA 564
QY 989 TACTAGTAATGAGAGATGAATATGATTTCAATCTTTGTAGTGTCTGTACTACTGTGC 1048
DB 565 TACTAGTAATGAGAGATGAATATGATTTCAATCTTTGTAGTGTCTGTACTACTGTGC 624
QY 1049 TGATCCGCGGTTATTTATTCATTTAGCGTTGCAACGAGACTTGCACAAAGATTCAGCATT 1108
DB 625 TGATCCGCGGTTATTTATTCATTTAGCGTTGCAACGAGACTTGCACAAAGATTCAGCATT 684
QY 1109 TGCTTCATTTAGGTAAT 1125
DB 685 TGCTTCATTTAGGTAAT 701
RESULT 12
AAH73816
ID AAH73816 standard; DNA; 1158 BP.
XX
XX AAH73816;
XX
XX 28-SEP-2001 (first entry)
XX
XX Potato patatin coding sequence.
XX
XX Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
XX larva growth; lipid acyl hydrolase; insecticide; ds.
XX
XX Solanum tuberosum.
XX
XX MO200149834-A2.
XX
XX 12-JUL-2001.
XX
XX 05-JAN-2001; 2001MO-US000342.
XX
XX 06-JAN-2000; 2000US-0174669P.
XX
XX (MONS) MONSANTO CO.
XX
XX Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA;
XX
XX MPI; 2001-441874/47.
XX
XX P-PSDB; AAG99079.
XX
XX Modified potato patatin proteins with reduced antigenicity, useful as
XX insecticides for controlling e.g. round worm and root worm.
XX
XX Example 5; Page 133-134; 223pp; English.
XX
XX The present invention relates to modified potato patatins that maintain
XX enzymatic and insecticidal activity but which have reduced allergenicity.
XX Groups (especially Tyr) which bind to anti-patatin antibodies were
XX identified and glycosylation sites involved in antibody binding were
XX removed via site directed mutagenesis. The patatins stunt the growth of
XX larvae so that maturation is prevented or delayed. The patatins also have
XX non-specific lipid acyl hydrolase activity. The modified patatins are
XX also useful for inhibiting the activity of corn round worms.
XX Deallergenised protein can be used as insecticides, as nutritional
XX supplements and as immunising agents. The present sequence was used to
XX illustrate the present invention
XX
XX Sequence 1158 BP; 380 A; 207 C; 221 G; 350 T; 0 U; 0 Other;
SQ
Query Match 59.5%; Score 671.4; DB 4; Length 1158;
Best Local Similarity 99.9%; Pred. No. 4.2e-169;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 453 CAGTTGGAGAAATGGTGACTGTTCTTAGATTGATGAGGATTTAGAGGATCATTT 512
DB 70 CAGTTGGAGAAATGGTGACTGTTCTTAGATTGATGAGGATTTAGAGGATCATTT 129

```
QY 513 CCGGCTACCATTCGCAATTTCTTGAAGACAATTGAGAAAATGCAATTAATGAGAT 572
DB 130 CCGGCTACCATTCGCAATTTCTTGAAGACAATTGAGAAAATGCAATTAATGAGAT 189
QY 573 GCAAGACTTGCAATTAATTTGATGATTAATGAGAAAATGCAATTAATGAGAT 632
DB 190 GCAAGACTTGCAATTAATTTGATGATTAATGAGAAAATGCAATTAATGAGAT 249
QY 633 GCAATTAATTAATTTGATGATTAATTTGATGATTAATTTGATGATTAATTTGAT 692
DB 250 GCAATTAATTAATTTGATGATTAATTTGATGATTAATTTGATGATTAATTTGAT 309
QY 693 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 752
DB 310 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 369
QY 753 AAATATGATGAAAATATCTTATGCAAGTTCTTCAAGAAAATTTGAGAAAATCTG 812
DB 370 AAATATGATGAAAATATCTTATGCAAGTTCTTCAAGAAAATTTGAGAAAATCTG 429
QY 813 CATCAAGCTTTGACAGAAAGTTGATCTCAAGCTTTGACATCAAAAATTAAGCCGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTTGATCTCAAGCTTTGACATCAAAAATTAAGCCGTA 489
QY 873 ATATTCCTAAGTCAATTTAGCAAACTCTCCAGAAATTTGATGATGATGATGATG 932
DB 490 ATATTCCTAAGTCAATTTAGCAAACTCTCCAGAAATTTGATGATGATGATGATG 549
QY 933 AGTTATTCACAGACAGAGCTCCCAATATTTCTCCGATTAATTTGATTAATTAAT 992
DB 550 AGTTATTCACAGACAGAGCTCCCAATATTTCTCCGATTAATTTGATTAATTAAT 609
QY 993 AGTTATTCAGATGAATATGATGATTAATTTGATGATGATGATGATGATGATG 1052
DB 610 AGTTATTCAGATGAATATGATGATTAATTTGATGATGATGATGATGATGATG 669
QY 1053 CCGGCGTTATTCATTAAGCTTTGCAAGAGCTTGCAAAAAGATCCAGCAATTTGCT 1112
DB 670 CCGGCGTTATTCATTAAGCTTTGCAAGAGCTTGCAAAAAGATCCAGCAATTTGCT 729
QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTCAT 742

RESULT 13
ADM93077
ID ADM93077 standard; DNA; 1158 BP.
XX
AC ADM93077;
XX
DT 03-JUN-2004 (first entry)
XX
DE Potato patatin DNA.
XX
KW lipid acyl hydrolase; corn rootworm; insect infestation; plant;
XX insect control; nutritional supplement; potato; patatin; de; Gene.
XX
OS Solanum tuberosum.
XX
PN US6657046-B1.
XX
PD 02-DEC-2003.
XX
PF 05-JAN-2001; 2001US-00755274.
XX
PR 06-JAN-2000; 2000US-0174669P.
XX 21-JUL-2000; 2000US-0219912P.
XX (MONS ) MONSANTO TECHNOLOGY LLC.
XX
XX Alibhai MF, Rydel TJ;
XX
PI
```

```
XX
DR WPI; 2004-058368/06.
DR P-PSDB; ADM93078.
XX
PT New lipid acyl hydrolase proteins, useful for inhibiting insect
PT infestation of a plant or plant part, for controlling insects, as
XX nutritional supplements, or in immunotherapy protocols.
XX
PS Disclosure; SEQ ID NO 38; 73pp; English.
XX
XX The invention relates to an isolated peptide exhibiting lipid acyl
XX hydrolase activity and corn rootworm insect inhibitory bioactivity. The
XX lipid acyl hydrolase peptide is useful for inhibiting insect infestation
XX of a plant or plant part, for controlling insects (e.g. corn rootworm),
XX as nutritional supplements, and in immunotherapy protocols. The present
XX sequence represents a potato patatin DNA.
XX
SQ Sequence 1158 BP; 380 A; 207 C; 221 G; 350 T; 0 U; 0 Other;
XX
Query Match 59.5%; Score 671.4; DB 12; Length 1158;
Best Local Similarity 99.9%; Pred. No. 4,2e-169;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 453 CAGTTGGAGAAAATGATGATCTGTTCTTATGATGATGATGATGATGATGATGAT 512
DB 70 CAGTTGGAGAAAATGATGATCTGTTCTTATGATGATGATGATGATGATGATGAT 129
QY 513 CCGGCTACCATTCGCAATTTCTTGAAGACAATTGAGAAAATGCAATTAATGAGAT 572
DB 130 CCGGCTACCATTCGCAATTTCTTGAAGACAATTGAGAAAATGCAATTAATGAGAT 189
QY 573 GCAAGACTTGCAATTAATTTGATGATTAATGAGAAAATGCAATTAATGAGAT 632
DB 190 GCAAGACTTGCAATTAATTTGATGATTAATGAGAAAATGCAATTAATGAGAT 249
QY 633 GCAATTAATTAATTTGATGATTAATTTGATGATTAATTTGATGATTAATTTGAT 692
DB 250 GCAATTAATTAATTTGATGATTAATTTGATGATTAATTTGATGATTAATTTGAT 309
QY 693 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 752
DB 310 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 369
QY 753 AAATATGATGAAAATATCTTATGCAAGTTCTTCAAGAAAATTTGAGAAAATCTG 812
DB 370 AAATATGATGAAAATATCTTATGCAAGTTCTTCAAGAAAATTTGAGAAAATCTG 429
QY 813 CATCAAGCTTTGACAGAAAGTTGATCTCAAGCTTTGACATCAAAAATTAAGCCGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTTGATCTCAAGCTTTGACATCAAAAATTAAGCCGTA 489
QY 873 ATATTCCTAAGTCAATTTAGCAAACTCTCCAGAAATTTGATGATGATGATGATG 932
DB 490 ATATTCCTAAGTCAATTTAGCAAACTCTCCAGAAATTTGATGATGATGATGATG 549
QY 933 AGTTATTCACAGACAGAGCTCCCAATATTTCTCCGATTAATTTGATTAATTAAT 992
DB 550 AGTTATTCACAGACAGAGCTCCCAATATTTCTCCGATTAATTTGATTAATTAAT 609
QY 993 AGTTATTCAGATGAATATGATGATTAATTTGATGATGATGATGATGATGATG 1052
DB 610 AGTTATTCAGATGAATATGATGATTAATTTGATGATGATGATGATGATGATG 669
QY 670 CCGGCGTTATTCATTAAGCTTTGCAAGAGCTTGCAAAAAGATCCAGCAATTTGCT 729
QY 1053 CCGGCGTTATTCATTAAGCTTTGCAAGAGCTTGCAAAAAGATCCAGCAATTTGCT 1112
DB 670 CCGGCGTTATTCATTAAGCTTTGCAAGAGCTTGCAAAAAGATCCAGCAATTTGCT 729
QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTCAT 742

RESULT 14
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AAH73854
 ID AAH73854 standard; DNA; 1161 BP.
 AC AAH73854;
 XX
 XX
 DT 28-SEP-2001 (first entry)
 DE Patatin homolog Pat17 coding sequence.
 XX
 XX Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
 KM larva growth; lipid acyl hydrolase; insecticide; ds.
 XX
 OS Solanum tuberosum.
 PN WO200149834-A2.
 PD 12-JUL-2001.
 PF 05-JAN-2001; 2001MO-US000342.
 PR 06-JAN-2000; 2000US-0174669P.
 PA (MONS) MONSANTO CO.
 XX
 PI Alibhai MF, Ashtwood JD, McWherter CA, Sampson HA;
 DR WPI; 2001-441874/47.
 XX
 PT Modified potato patatin proteins with reduced antigenicity, useful as
 XX insecticides for controlling e.g. round worm and root worm.
 PS Disclosure; Page 210-211; 223pp; English.
 XX
 CC The present invention relates to modified potato patatins that maintain
 CC enzymatic and insecticidal activity but which have reduced allergenicity.
 CC Groups (especially Tyr) which bind to anti-patatin antibodies were
 CC identified and glycosylation sites involved in antibody binding were
 CC removed via site directed mutagenesis. The patatins stunt the growth of
 CC larvae so that maturation is prevented or delayed. The patatins also have
 CC non-specific lipid acyl hydrolase activity. The modified patatins are
 CC also useful for inhibiting the activity of corn round worms.
 CC Deallergerised protein can be used as insecticides, as nutritional
 CC supplements and as immunising agents. The present sequence was used to
 CC illustrate the present invention
 CC
 SQ Sequence 1161 BP; 382 A; 207 C; 221 G; 351 T; 0 U; 0 Other;
 Query Match 59.5%; Score 671.4; DB 4; Length 1161;
 Best Local Similarity 99.9%; Pred. No. 4.2e-169;
 Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 453 CAGTTGGAGAAATGCTGTTCTTATGATGAGTGAATTAAGGATCAT 512
 DB 70 CAGTTGGAGAAATGCTGTTCTTATGATGAGTGAATTAAGGATCAT 129
 QY 513 CCGGCTACCATTCGATTTCTTGAAGCAACTTCAGAAATGCAATTAATGAT 572
 DB 130 CCGGCTACCATTCGATTTCTTGAAGCAACTTCAGAAATGCAATTAATGAT 189
 QY 573 GCAAGCTTGCAATTAATTCGATTTGAAGCAAGTACAGAGCTTATGACT 632
 DB 190 GCAAGCTTGCAATTAATTCGATTTGAAGCAAGTACAGAGCTTATGACT 249
 QY 633 GCTATGATAGTACTCCAAATGAAACATGACCTTCTCTGCGCAAAATTTGA 692
 DB 250 GCTATGATAGTACTCCAAATGAAACATGACCTTCTCTGCGCAAAATTTGA 309
 QY 693 CTTTTTACTTGAACATGCGCTCAGATTTTAACTTCAAGTCAATTTTAAAGCCCA 752
 DB 310 CTTTTTACTTGAACATGCGCTCAGATTTTAACTTCAAGTCAATTTTAAAGCCCA 369
 QY 753 AATATGATGAAATATCTTATGCAAGTTCTTCAAGAAATCTGAGAAATCTGCTG 812

DB 370 AATATGATGAAATATCTTATGCAAGTTCTTCAAGAAATCTGAGAAATCTGCTG 429
 QY 813 CATCAAGCTTTGACAGAACTTGATCTCAAGCTTTGACATCAAAACAATTAAGCCAGTA 872
 DB 430 CATCAAGCTTTGACAGAACTTGATCTCAAGCTTTGACATCAAAACAATTAAGCCAGTA 489
 QY 873 ATATTGATGAAATTTAGCAACTCTCCAGATTTGATGATGATGATGATGATGATGATGAT 932
 DB 490 ATATTGATGAAATTTAGCAACTCTCCAGATTTGATGATGATGATGATGATGATGATGAT 549
 QY 933 AGTTATTCACAGACAGACCTCCAAATTTTCCCTCCGATTAATCTTTTAATTAAT 992
 DB 550 AGTTATTCACAGACAGACCTCCAAATTTTCCCTCCGATTAATCTTTTAATTAAT 609
 QY 993 AGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
 DB 610 AGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
 QY 1053 CCGGCTTATTTATCCATTTGCGTTGCAAGACCTTGCAAGACCTTGCAAGACCTTGCAAG 1112
 DB 670 CCGGCTTATTTATCCATTTAGCGTTGCAAGACCTTGCAAGACCTTGCAAGACCTTGCAAG 729
 QY 1113 TCAATTAGGTAAT 1125
 DB 730 TCAATTAGGTCAT 742
 RESULT 15
 ADM93076
 ID ADM93076 standard; DNA; 1161 BP.
 XX
 AC ADM93076;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Heartleaf nightshade patatin homologue Pat17 DNA.
 XX
 KM lipid acyl hydrolase; corn rootworm; insect infestation; plant;
 KM insect control; nutritional supplement; heartleaf nightshade; patatin;
 XX Pat17; ds; gene.
 XX
 OS Solanum cardiophyllum.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1161
 FT /tag= a
 FT /product= "Pat17"
 XX
 PN US6657046-B1.
 XX
 PD 02-DEC-2003.
 PF 05-JAN-2001; 2001US-00755274.
 PR 06-JAN-2000; 2000US-0174669P.
 PR 21-JUL-2000; 2000US-0219912P.
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Alibhai MF, Rydel TJ,
 XX
 DR WPI; 2004-058368/06.
 DR P-PSDB; ADM93040.
 XX
 PT New lipid acyl hydrolase proteins, useful for inhibiting insect
 PT infestation of a plant or plant part, for controlling insects, as
 PT nutritional supplements, or in immunotherapy protocols.
 XX
 PS Example 1; SEQ ID NO 37; 73bp; English.
 XX
 CC The invention relates to an isolated peptide exhibiting lipid acyl
 CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The
 CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation

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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 13:10:45 ; Search time 3611 Seconds
(without alignments)
11890.472 Million cell updates/sec

Title: US-10-658-180-246

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 619.8 | 54.9 | 893 | 7 | CV471846 45073.1 C |
| 4 | 619.8 | 54.9 | 908 | 7 | CV472569 45932.1 C |
| 5 | 619.8 | 54.9 | 950 | 7 | CV470623 43531.1 C |
| 6 | 619.8 | 54.9 | 973 | 7 | CV469887 42645.1 C |
| 7 | 618.8 | 54.9 | 736 | 4 | BG351688 131A01 Ma |
| 8 | 618.2 | 54.8 | 756 | 4 | BG887880 EST513731 |
| 9 | 618.2 | 54.8 | 802 | 4 | BG351001 099E05 Ma |
| 10 | 618.2 | 54.8 | 828 | 4 | BG351741 131G03 Ma |
| 11 | 617.4 | 54.7 | 819 | 7 | CV469997 42774.1 C |
| 12 | 617.2 | 54.7 | 741 | 4 | BG351249 088C08 Ma |
| 13 | 616.8 | 54.7 | 700 | 4 | BG351792 132G04 Ma |
| 14 | 616.6 | 54.7 | 781 | 4 | BG887154 EST513005 |
| 15 | 616.4 | 54.6 | 795 | 7 | CV286460 66740.1 A |
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| 18 | 616.4 | 54.6 | 815 | 7 | CV470351 43196.1 C |
| 19 | 616.4 | 54.6 | 823 | 4 | BG350911 085C06 Ma |
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| 21 | 616.4 | 54.6 | 909 | 7 | CV471819 45044.1 C |
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| 23 | 615.4 | 54.6 | 687 | 4 | BG350408 091B04 Ma |
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| 27 | 613.6 | 54.4 | 738 | 4 | BI406184 156G03 Ma |
| 28 | 613.6 | 54.4 | 861 | 7 | CV470821 43768.1 C |
| 29 | 613.4 | 54.4 | 765 | 7 | CV469493 42153.1 C |
| 30 | 612.8 | 54.3 | 741 | 4 | BG351882 135B05 Ma |
| 31 | 612.4 | 54.3 | 744 | 7 | CV286462 66742.1 A |
| 32 | 610.6 | 54.1 | 708 | 4 | BG351129 087H07 Ma |
| 33 | 610.2 | 54.1 | 755 | 4 | BG351082 087G03 Ma |
| 34 | 610.2 | 54.1 | 812 | 4 | BG351121 087G05 Ma |
| 35 | 610.2 | 54.1 | 828 | 4 | BG351737 131F09 Ma |
| 36 | 609.6 | 54.0 | 780 | 7 | CV472434 45776.1 C |
| 37 | 609 | 54.0 | 683 | 4 | BI405724 115E09 Ma |
| 38 | 608.8 | 54.0 | 862 | 7 | CV469304 41917.1 C |
| 39 | 608.8 | 54.0 | 946 | 7 | CV471010 43986.1 C |
| 40 | 608.6 | 54.0 | 702 | 4 | BG351774 132D09 Ma |
| 41 | 608.6 | 54.0 | 713 | 4 | BI435957 EST538718 |
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| 43 | 608.6 | 54.0 | 763 | 7 | CV472232 45537.1 C |
| 44 | 608.6 | 54.0 | 812 | 7 | CV468931 41376.1 C |
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ALIGNMENTS

RESULT 1
BG351670 813 bp mRNA linear EST 11-SEP-2002
LOCUS 130E12 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
DEFINITION BG351670
ACCESSION BG351670
VERSION BG351670.1 GI:13180412
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 813)
Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.
The potato tuber transcriptome: analysis of 6077 expressed sequence
tags
FEBS Lett. 506 (2), 123-126 (2001)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Karen G. Welinder
Instituit for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 813
POLYA-No.

FEATURES
Source
1. 813
/organism="Solanum tuberosum"
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/db_xref="taxon:4113"
/tissue_type="Tuber"
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/note="Vector: lambda ZAP"

ORIGIN

Query Match 54.9%; Score 619.8; DB 4; Length 813;
Best Local Similarity 95.2%; Pred. No. 1.2e-150;
Matches 639; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 455 GTTGGAGGAATGAGTCTTCTTAGTATTGATGAGGTGAGGATTTAGAGGATCATTC 514
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Db      74 GTTGGAGAAATGCTGACTTCTTCTAGTATTGATGAGAGTGGAATTAAGGAATCATTC 133
QY      515 GGCTACCAATTCCTGCAATTTCTTGAGAGCAACTTCAGAAATGAGACATTAATGACAGATGC 574
Db      134 GGCTACCAATTCCTGCAATTTCTTGAGAGCAACTTCAGAGAGTGGAACATTAATAAGATGC 193
QY      575 AAGACTTGAGATTAATCTTGAATGTAATTTGAGAGCAAGTACAGAGAGTTTATTGACTGC 634
Db      194 AAGACTTGAGATTAATCTTGAATGTAATTTGAGAGCAAGTACAGAGAGTTTATTGACTGC 253
QY      635 TATGATAGTACTCCAAATGAAAAACAATGACCTTTGCTGCTGCCAAGAAATTTGATCC 694
Db      254 TATGATAGTACTCCAAATGAAAAACAATGACCTTTGCTGCTGCCAAGAAATTTGATCC 313
QY      695 TTTTAACTTGCAACATGCGCTCGATGTTTAAATCTTGAATGTTTAAATTTGAGCCCAAA 754
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QY      755 ATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAAATCTGTGTGCA 814
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Db      614 TAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 673
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QY      1115 AATTAGTAAT 1125
Db      734 AATTAGTAAT 744

RESULT 2
CV471981      836 bp      mRNA      linear      EST 01-OCT-2004
LOCUS         45241.1 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone
DEFINITION   45241.1 mRNA sequence.
ACCESSION    CV471981
VERSION      CV471981.1 GI:53696757
KEYWORDS     EST.
SOURCE       Solanum tuberosum (potato)
ORGANISM     Solanum tuberosum
REFERENCE    1 (bases 1 to 836)
AUTHORS      Flihm,B., Rothwell,C., Sardana,R., Griffiths,R., Laguer,M., De
              Koeijer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.
TITLE        Generation of ESTs from common scab-challenged potato tubers
JOURNAL      Unpublished (2004)
COMMENT      Contact: Barry Flihm
              The Canadian Potato Genome Project - BioCplantech
              921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
              Email: bflim@biocplantech.mb.ca
              Seq primer: T3.
              Location/Qualifiers
                1..836
                /organism="Solanum tuberosum"

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/mol type="mRNA"
/cultivar="Shepody"
/db xref="taxon:4113"
/clone="45241"
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/lab host="X110-Gold"
/clone lib="Common Scab-Challenged Tubers"
/notes="Vector: pBluescript II SK(+). XR Site 1: EcoRI;
Site 2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with Streptomyces scabiei EF-35, by
applying 1 ml of a spore stock (OD650 = 0.7). Tubers were
placed in trays of sand and watered from the bottom for
the remainder of the experiment. Inoculated tubers were
sampled at 2 days, 1 week, 2 weeks and 4 weeks
post-infection. Harvested tubers were washed in distilled
water, blotted dry, cut into small pieces and frozen in
liquid nitrogen. RNA was isolated from each sample
collection, pooled and used for cDNA library
construction."

ORIGIN
Query Match      54.9%; Score 619.8; DB 7; Length 836;
Best Local Similarity 95.2%; Pred. No. 1,2e-150;
Matches 639; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

455 GTTGGAGAAATGCTGACTGTTCTTATGATGATGAGAGTGGAATTAAGGATCATTC 514
Db      89 GTTGGAGAAATGCTGACTGTTCTTATGATGATGAGAGTGGAATTAAGGATCATTC 148
QY      515 GGCTACCAATTCCTGCAATTTCTTGAGAGCAACTTCGAGAAATGAGCAATTAAGCAATGC 574
Db      149 GGCTACCAATTCCTGCAATTTCTTGAGAGCAACTTCGAGAAATGAGCAATTAAGCAATGC 208
QY      575 AAGACTTGAGATTAATCTTGAATGTAATTTGAGAGCAAGTACAGAGAGTTTATTGACTGC 634
Db      209 AAGACTTGAGATTAATCTTGAATGTAATTTGAGAGCAAGTACAGAGAGTTTATTGACTGC 268
QY      635 TATGATAGTACTCCAAATGAAAAACAATGACCTTTGCTGCTGCCAAGAAATTTGATCC 694
Db      269 TATGATAGTACTCCAAATGAAAAACAATGACCTTTGCTGCTGCCAAGAAATTTGATCC 328
QY      695 TTTTAACTTGCAACATGCGCTCGATGTTTAAATCTTGAATGTTTAAATTTGAGCCCAAA 754
Db      329 TTTTAACTTGCAACATGCGCTCGATGTTTAAATCTTGAATGTTTAAATTTGAGCCCAAT 388
QY      755 AATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAAATCTGTGTGCA 814
Db      389 AATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAGAAAATCTGTGTGCA 448
QY      815 TCAAGCTTTGACAGAGTTGTCTCATCTCAAGCTTTGACATCAAAACAATTAAGCAATAT 874
Db      449 TCAAGCTTTGACAGAGTTGTCTCATCTCAAGCTTTGACATCAAAACAATTAAGCAATAT 508
QY      875 ATTCACTTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGCTAAGATGATGACATAG 934
Db      509 ATTCACTTAAGTCAAAATTTAGCAAACTCTCCAGAAATTTGATGCTAAGATGATGACATAG 568
QY      935 TTATTCACAGCAGCAGCTCCAAATTTTCTCCGCAATTAATTTGATTAATTAATAG 994
Db      569 TTATTCACAGCAGCAGCTCCAAATTTTCTCCGCAATTAATTTGATTAATTAATAG 628
QY      995 TAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1054
Db      629 TAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
QY      1055 GGGCTTATTAATCAATTAAGCGTTGCAACAGAGCTTGCAAAAGAGATCCAGATTTGCTTC 1114
Db      689 GGGCTTATTAATCAATTAAGCGTTGCAACAGAGCTTGCAAAAGAGATCCAGATTTGCTTC 748
QY      1115 AATTAGTAAT 1125
Db      749 AATTAGTAAT 759

```

| RESULT 3 | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM | REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT | FEATURES |
|--|----------------|--|-----------|------------|-------------|--------|----------|-----------|---------|-------|---------|---------|----------|
| Cv471846 | 983 bp | mRNA | linear | EST | 01-OCT-2004 | | | | | | | | |
| Cv471846 | 45073.1 | Common Scab-Challenged Tubers Solanum tuberosum cDNA clone | | | | | | | | | | | |
| Cv471846 | 45073.5 | mRNA sequence. | | | | | | | | | | | |
| Cv471846.1 | GI:53696622 | EST. | | | | | | | | | | | |
| Solanum tuberosum (potato) | | | | | | | | | | | | | |
| Solanum tuberosum | | | | | | | | | | | | | |
| Eubacteriales; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanales; Solanaceae; Solanum. | | | | | | | | | | | | | |
| 1 (bases 1 to 893) | | | | | | | | | | | | | |
| Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Laque, M., De Koeper, D., Andy, P., Goyer, C., Li, X.-Q., Wang, P., Skl, G., and Regan, S. | | | | | | | | | | | | | |
| Generation of ESTs from common scab-challenged potato tubers | | | | | | | | | | | | | |
| Unpublished (2004) | | | | | | | | | | | | | |
| Contact: Barry Flinn | | | | | | | | | | | | | |
| The Canadian Potato Genome Project - BioAtlantech | | | | | | | | | | | | | |
| 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA | | | | | | | | | | | | | |
| Email: bflinn@bioatlantech.nb.ca | | | | | | | | | | | | | |
| Seq primer: T3. | | | | | | | | | | | | | |
| Location/Qualifiers | | | | | | | | | | | | | |
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| /cultivar="Shepody" | | | | | | | | | | | | | |
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| /lab_host="XL10-Gold" | | | | | | | | | | | | | |
| /clone_lib="Common Scab-Challenged Tubers" | | | | | | | | | | | | | |
| /note="Vector: pBluescript II SK(+); XR; Site 1: EcoRI; Site 2: XhoI; supplier: Pathogen-challenge berries. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with Streptomyces scabEI EF-35, by applying 1 ml of a spore stock (OD650 = 0.7). Tubers were placed in trays of sand and watered from the bottom for the remainder of the experiment. Inoculated tubers were sampled at 2 days, 1 week, 2 weeks and 4 weeks post-infection. Harvested tubers were washed in distilled water, blotted dry, cut into small pieces and frozen in liquid nitrogen. RNA was isolated from each sample collection, pooled and used for cDNA library construction." | | | | | | | | | | | | | |
| ORIGIN | | | | | | | | | | | | | |
| Query Match | 54.9% | Score 619.8 | DB 7 | Length 893 | | | | | | | | | |
| Best Local Similarity | 95.2% | Pred. No. 1.2e-150 | | | | | | | | | | | |
| Matches 639 | Conservative 0 | Mismatches 32 | Indels 0 | Gaps 0 | | | | | | | | | |
| 455 GTTGGGAAGAAAGGACGCTGTTCTTAGATTGATGAGGTGGAATTAGAGGATCATCC | 514 | | | | | | | | | | | | |
| Db 76 GTTGGGAAGAAAGGACGCTGTTCTTAGATTGATGAGGTGGAATTAGAGGATCATCC | 135 | | | | | | | | | | | | |
| 515 GGCTACCAATTCGCAATTCCTTGAAGACAACCTCAGAAATGACAATATGACAGATGC | 574 | | | | | | | | | | | | |
| Db 136 GGCTACCAATTCGCAATTCCTTGAAGACAACCTCAGAAATGACAATATGACAGATGC | 195 | | | | | | | | | | | | |
| 575 AAGACTTGCAATTCCTTGAATGATGATGATGAGGAAACAATGACAGAGGTTATGACTGC | 634 | | | | | | | | | | | | |
| Db 196 AAGACTTGCAATTCCTTGAATGATGATGAGGAAACAATGACAGAGGTTATGACTGC | 255 | | | | | | | | | | | | |
| 635 TATGATAGTACTCCAAATGAAACAATGACACCTTTGCTGCTGCAAGAATATGATACC | 694 | | | | | | | | | | | | |
| Db 256 TATGATAGTACTCCAAATGAAACAATGACACCTTTGCTGCTGCAAGAATATGATACC | 315 | | | | | | | | | | | | |

| REFERENCE | TITLE | JOURNAL | COMMENT |
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| 755 | ATATGATGAGAAAATATCTTATGTGCAAGTTCTTCAAGAAAACTTGGAGAAA | CTGCTGTGCA | 814 |
| 376 | GTATGATGAGAAAATATTTTCTGCAAGTTCTTCAAGAAAACTTGGAGAAA | CTGCTGTGCA | 435 |
| 815 | TCAGACTTTTGCACAGAGTTGTCAATCTCAAGCTTTGACATCAAAACAATTA | AGCAGTAAT | 874 |
| 436 | TCAGACTTTTGCACAGAGTTGTCAATCTCAAGCTTTGACATCAAAACAATTA | AGCAGTAAT | 495 |
| 875 | ATTGACTTAAGCAAAATTAGCAAACTCTCCAGAAATTGGATGCTAAGATGTA | GTACATAG | 934 |
| 496 | ATTGACTTAAGCAAAATTAGCAAACTCTCCAGAAATTGGATGCTAAGATGTA | GTACATAG | 555 |
| 935 | TTATTTCCACAGACAGACCTCCACATATTTTCCCTCCGATTAATCTTTACTA | TACTAG | 994 |
| 556 | TTATTTCCACAGACAGACCTCCACATATTTTCCCTCCGATTAATCTTTACTA | TACTAG | 615 |
| 995 | TTAATGAGATGATATATGATTCATCTTGTGTATGTGTGCTGTCTA | CTGTGATCC | 1054 |
| 616 | TTAATGAGATGATATATGATTCATCTTGTGTATGTGTGCTGTCTA | CTGTGATCC | 675 |
| 1055 | GGCGTTTATTCATCTTGTGTATGTGTGCTGTCTA | CTGTGATCC | 1114 |
| 676 | GGCGTTTATTCATCTTGTGTATGTGTGCTGTCTA | CTGTGATCC | 735 |
| 1115 | AATTAGGTAAT | 1125 | |
| 736 | AATTAGGTAAT | 746 | |
| RESULT 4 | | | |
| CV472569 | 908 bp | mRNA | linear |
| LOCUS | EST 01-OCT-2004 | | |
| DEFINITION | 45932.1 Common Scab-Challenged Tubers Solanum tuberosum | cDNA clone | |
| ACCESSION | 45932.5 | mRNA sequence. | |
| VERSION | CV472569 | | |
| KEYWORDS | CV472569.1 | GI:53697345 | |
| SOURCE | EST. | | |
| ORGANISM | Solanum tuberosum (potato) | | |
| | Solanum tuberosum | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; | | |
| | asterids; lamiales; Solanales; Solanaceae; Solanum. | | |
| | 1 (bases 1 to 908) | | |
| | Flinn, B., Roehwell, C., Sardana, R., Griffiths, R., Laque, M., De | | |
| | Koeper, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G., and Regan, S. | | |
| | Generation of ESTs from common scab-challenged potato tubers | | |
| | Unpublished (2004) | | |
| | Contact: Barry Flinn | | |
| | The Canadian Potato Genome Project - BioAtlantech | | |
| | 921 Collège Hill Rd, Fredericton, ON, E3B 6Z9, CANADA | | |
| | Email: bflinn@bioatlantech.nb.ca | | |
| | Seq primer: T3. | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..908 | | |
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| | /db_xref="taxon:4113" | | |
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| | /issue_type="Tubers" | | |
| | /lab_host="XLI10-Gold" | | |
| | /clone_1lb="Common Scab-Challenged Tubers" | | |
| | /note="Vector: pBluescript II SK(+), XR, Site_1: EcoRI, Site_2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with Streptomyces scabiei Er-35, by applying 1 ml of a spore stock (OD650 = 0.7). Tubers were placed in trays of sand and watered from the bottom for the remainder of the experiment. Inoculated tubers were sampled at 2 days, 1 week, 2 weeks and 4 weeks post-infection. Harvested tubers were washed in distilled water, blotted dry cut into small pieces and frozen in | | |

| | | | |
|----|------|---|------|
| Qy | 995 | TAATGAGATAAATGATGTTCAATCTGTGATGATGTCGTGGCTACTGTGTGATGCC | 1054 |
| Db | 608 | TAATGAGATAAATGATGTTCAATCTGTGATGATGTCGTGGCTACTGTGTGATGCC | 667 |
| Qy | 1055 | GGCGTTATTCATTCATTAGCGTTGCACAGACTTGCAAAAAGATTCAGACTTTC | 1114 |
| Db | 668 | GGCGTTATTCATTCATTAGCGTTGCACAGAACTTGCAAGTGATCCAAATTTC | 727 |
| Qy | 1115 | AATTAGGTAAT | 1125 |
| Db | 728 | AATTAGGTAAT | 738 |

| | | | | | |
|------------|--|------------|------|--------|-----------------|
| RESULT 6 | CVA69887 | 973 bp | mRNA | linear | EST 01-OCT-2004 |
| LOCUS | CVA69887 | | | | |
| DEFINITION | CVA69887 42645.1 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone 42645 5', mRNA sequence. | | | | |
| ACCESSION | CVA69887 | | | | |
| VERSION | CVA69887.1 | GI:5369463 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Solanum tuberosum (potato) | | | | |
| ORGANISM | Solanum tuberosum | | | | |

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

| REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|----------------------|---|--|--------------------|---------|
| 1. (bases 10 to 973) | Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De Koeper, D., Audy, P., Goyer, C., Li, X-Q., Wang-Pruski, G. and Regan, S. | Generation of ESRs from common scab-challenged potato tubers | Unpublished (2004) | |
| | Contact: Barry Flinn | | | |

The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

| FEATURES | Location/Qualifiers |
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/clone_lib="Common Scab-Challenged Tubers"
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Site 2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with Streptomyces scabiei EF-35, by
applying 1 ml of a spore stock (OD650 = 0.7). Tubers were
placed in trays of sand and watered from the bottom for
the remainder of the experiment. Inoculated tubers were
sampled at 2 days, 1 week, 2 weeks and 4 weeks
post-infection. Harvested tubers were washed in distilled
water, blotted dry, cut into small pieces and frozen in
liquid nitrogen. RNA was isolated from each sample
collection, pooled and used for cDNA library
construction."

```

| | | | | |
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| Query Match | 54.9%; | Score 619.8; | DB 7; | Length 973; |
| Best Local Similarity | 95.2%; | Pred. No. 1.2e-150; | | |
| Matches 639; Conservative | 0; | Mismatches 32; | Indels 0; | Gaps 0. |

| QY | QY | QY | QY |
|-----|---|--|-----|
| 455 | GTGGGGAAGAAATGGGACGCTTTCTTAAGTATGATGAGGTGGAAATTAGAGGATCATATCC | 514 | |
| 68 | GTGGGAGAAATGGGACGCTTTCTTAAGTATGATGAGGTGGAAATTAGAGGATCATATCC | 127 | |
| QY | 515 | GGCTACCATTTCTCGAAATTTCTTGAAGGACAACTTCAGGAAATGGACATTAATGCGATGTC | 574 |
| Db | 128 | GGCTACCATTTCTCGAAATTTCTTGAAGGACAACTTCAGGAAATGGGACATTAATTAAGATGTC | 187 |

| | | | | | | | |
|----|------|----------------|---------------|-----------------|----------------------------|---------------------|------|
| QY | 575 | AAGCTTCGAGATTA | CTTGATGTAAAT | TGGAGAAACA | GTACAGAGAGTTAT | TGACATGC | 634 |
| Db | 188 | AAGCTTCGAGATTA | CTTGATGTAAAT | TGGAGAAACA | GTACAGAGAGTTAT | TGACATGC | 247 |
| QY | 635 | TATGATTAAGTAC | TCGAAATGAAA | CAATCGACCC | TTTGCTGCTGCC | CAAGAAATTTGATCC | 694 |
| Db | 248 | TATGATTAAGTAC | TCGAAATGAAA | CAATCGACCC | TTTGCTGCTGCC | CAAGAAATTTGATCC | 307 |
| QY | 695 | TTTTTACTCGA | AATGGCCCTCGA | TTTTTAACT | AGTGGTCAAA | TTTTTAAAGGCCAAA | 754 |
| Db | 308 | TTTTTACTCGA | AATGGCCCTCGA | TTTTTAACT | AGTGGTCAAA | TTTTTAAAGGCCAAT | 367 |
| QY | 755 | ATTATGATGAAA | AATATCTTA | TGCAAGTCTT | CAAGAAAA | CTTGGAGAACTCGTGTGCA | 814 |
| Db | 368 | GTAATGATGAAA | AATATCTT | TCGCAAGTCTT | CAAGAAAA | CTTGGAGAACTCGTGTGCA | 427 |
| QY | 815 | TCAGAGTTTGA | CAGAAGTGTGAT | CTCAGCTT | GACATCAAA | CAAAATTAAGCCAGTAT | 874 |
| Db | 428 | TCAGAGTTTGA | CAGAAGTGTGAT | CTCAGCTT | GACATCAAA | CAAAATTAAGCCAGTAT | 487 |
| QY | 875 | ATTCACTA | TAGCAAAATTTAG | CAAACTTCCGAA | TTTGGATGCTAAGATGTATGACATAG | | 934 |
| Db | 488 | ATTCACTA | TAGCAAAATTTAG | CAAACTTCCGAA | TTTGGATGCTAAGATGTATGACATAG | | 547 |
| QY | 935 | TTATTCACAG | CAGACAGCTCC | CAATATTTTTCC | TCCGCACTTA | CTTTGTACTAATTA | 994 |
| Db | 548 | TTATTCACAG | CAGACAGCTCC | CAATATTTTTCC | TCCGCACTTA | CTTTGTACTAATTA | 607 |
| QY | 995 | TAATGAGATGA | ATATGAGTCAAT | CTTGTGTGAT | GTAGTGTGCTGCTA | CTGTGCTGATCC | 1054 |
| Db | 608 | TAATGAGATGA | ATATGAGTCAAT | CTTGTGTGAT | GTAGTGTGCTGCTA | CTGTGCTGATCC | 667 |
| QY | 1055 | GGCGTTATTA | TATCCATTAG | CGTTGCAAGAGACTT | GCAAAAGATCC | AGATTTGGCTTC | 1114 |
| Db | 668 | GGCGTTATTA | TATCCATTAG | CGTTGCAAGAGACTT | GCAAAAGATCC | AGATTTGGCTTC | 727 |
| QY | 1115 | AATTAGGTAAT | | 1125 | | | |
| Db | 728 | AATTAGGTAAT | | 738 | | | |

| | | | |
|-------------------|---|--------|-----------------------------|
| RESULT | | 7 | |
| LOCUS | BG351688 | | |
| DEFINITION | BG351688 | 736 bp | mRNA linear EST 11-SEP-2002 |
| ACCESSION | J13A01 Mature tuber lambda ZAP Solanum tuberosum cDNA, | | mRNA sequence. |
| VERSION | BG351688 | | |
| KEYWORDS | BG351688..1 GI:13180430 | | |
| SOURCE | EST. | | |
| ORGANISM | Solanum tuberosum (potato) | | |
| | Solanum tuberosum | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| | Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; | | |
| | Asterids; Lamiales; Solanales; Solanales; Solanales; Solanaceae; Solanum. | | |
| | 1 (bases 1 to 736) | | |
| REFERENCE AUTHORS | Crookshanks,M., Emmersen,U., Welinder,K.G. and Nielsen,K.L. | | |
| TITLE | The potato tuber transcriptome: analysis of 6077 expressed sequence | | |
| | tags | | |
| JOURNAL | FEMS Lett. 506 (2), 123-126 (2001) | | |
| MEDLINE | 21475600 | | |
| PUBMED | 11591384 | | |
| COMMENT | Contact: Karen G. Welinder | | |

ADDRESS Aalborg Universitet,
 Søndergade 13, 49, 9000 Aalborg, Denmark
TEL Tel.: +45 96358467
FAX Fax: +45 98141808
E-MAIL Email: kxw@bio.auc.dk
SEQUENCING Sequenced from the 5' end.
QUALITY High quality sequence stop: 736
POLYA-NO. POLYA=No.
FEATURES Location/Qualifiers
SOURCE 1..736


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Db      554 TTATTCACAGCAGCAGCTCCACATATTTTCCCTCCACATTTGTTACTGATACAG 613
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Qy      1055 GGGCTTATATTCATTCATTCAGCTTGCAAGAGCTTGCACAAAAGAGATCCAGATTGCTTC 1114
Db      674 CGGCTTATATTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC 733
Qy      1115 AATTAGTAT 1125
Db      734. AATTAGTAT 744

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LOCUS 099805 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
DEFINITION
ACCESSION BG351001 GI:13179727
VERSION BG351001.1
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
steroids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 802)
Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.
The potato tuber transcriptome: analysis of 6077 expressed sequence
tags
FEBS Lett. 506 (2), 123-126 (2001)

JOURNAL
MEDLINE 21475600
PUBMED 11591384
COMMENT Contact: Karen G. Welinder
Institute for biotechnology
Aalborg Universitet
Sohngaardsholmvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kye@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 802
POLYA=No.

FEATURES
source location/Qualifiers
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/organism="Solanum tuberosum"
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/cultivar="Field grown Kuras"
/tissue_type="tuber"
/clone_id="Mature tuber lambda ZAP"
/note="Vector: Lambda ZAP"

ORIGIN
Query Match 54.8%; Score 618.2; DB 4; Length 802;
Best Local Similarity 95.1%; Pred. No. 3,1e-150;
Matches 638; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy      455 GTTGGAGAGAAATGCTGCTGTTCTTACTATTTGAGAGCTGGAATTAGAGGATCATTC 514
Db      67 GTTGGAGAGAAATGCTGCTGTTCTTACTATTTGAGAGCTGGAATTAGAGGATCATTC 126
Qy      515 GGTACCATTCCTGCAATTTCTTGAAGACAACCTTCAGAAATGACATATATGACAGATGC 574
Db      127 GGTACCATTCCTGCAATTTCTTGAAGACAACCTTCAGAGAGTGAACATATAAGATGC 186
Qy      575 AAGACTTGCACTTCTTGTATTTGATTTGAGAGACAAGTACAGAGAGTTTATTGACTGC 634
Db      187 AAGACTTGCACTTCTTGTATTTGATTTGAGAGACAAGTACAGAGAGTTTATTGACTGC 246

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Qy      635 TATGATAGTACTCCAAATGAAAAACATCGACCTTTGCTGTCGCCAAGAAATTGTACC 694
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Db      307 TTTTACTTGGAACATGCGCCCTGAGATTTTAACTCTAGTGTCAATTTTAAAGCCCAA 366
Qy      755 ATATGATGAGAAATATTTTATGCAAGTCTTCAAGAAAACTTGAGAAACTGGTGTGA 814
Db      367 ATATGATGAGAAATATTTTCTGCAAGTCTTCAAGAAAACTTGAGAAACTGGTGTGA 426
Qy      815 TCAAGCTTTGACAGAAAGTGTCAATCTTCAGACTTTGACATCAAAACAATTAAGCCGTAAT 874
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Qy      875 ATTCACTAGTCAAAATTTAGCAAACTCTCCAGAAATGATGCTTAAGTATGACATTAAG 934
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Qy      935 TTATTCACAGCAGCAGCTCCACATATTTTCCCTCCGATTTACTTTGTTACTATACAG 994
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Qy      1055 GGGCTTATATTCATTCATTCAGCTTGCAAGAGCTTGCACAAAAGAGATCCAGATTGCTTC 1114
Db      667 GGGCTTATATTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC 726
Qy      1115 AATTAGTAT 1125
Db      727 AATTAGTAT 737

RESULT 10
BG351741 828 bp mRNA linear EST 11-SEP-2002
LOCUS 131603 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
DEFINITION
ACCESSION BG351741
VERSION BG351741.1 GI:13180483
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
steroids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 828)
Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.
The potato tuber transcriptome: analysis of 6077 expressed sequence
tags
FEBS Lett. 506 (2), 123-126 (2001)

JOURNAL
MEDLINE 21475600
PUBMED 11591384
COMMENT Contact: Karen G. Welinder
Institute for biotechnology
Aalborg Universitet
Sohngaardsholmvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kye@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 828
POLYA=No.

FEATURES
source location/Qualifiers
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/organism="Solanum tuberosum"
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/db_xref="taxon:4113"
/cultivar="Field grown Kuras"

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QY 1055 GGGGTATATATCATTTAGCGTTGCAAGACATTTGCAAAAAGATTCAGCATTTGCTTC 1114
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|
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|
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QY 1115 AATTAGG 1121
|
|
|
Db 748 AATTAGG 754
|
|
|
RESULT 12
BG351249 741 bp mRNA linear EST 11-SEP-2002
LOCUS 088C08 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
DEFINITION
ACCESSION BG351249
VERSION BG351249 GI:13179991
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 741)
Crookshank, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.
The potato tuber transcriptome: analysis of 6077 expressed sequence
tags
JOURNAL FEBS Lett. 506 (2), 123-126 (2001)
MEDLINE 21475600
PUBMED 11591384
COMMENT Contact: Karen G. Welinder
Institute for Biotechnology
Aalborg Universitet
Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 741
POLYA=No.
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VERSION BG351792.1 GI:13180534
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asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 700)
Crookshank, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.
The potato tuber transcriptome: analysis of 6077 expressed sequence
tags
JOURNAL FEBS Lett. 506 (2), 123-126 (2001)
MEDLINE 21475600
PUBMED 11591384
COMMENT Contact: Karen G. Welinder
Institute for Biotechnology
Aalborg Universitet
Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk
Sequenced from the 5' end.
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| Best Local Similarity | 95.2% | Pred. | No. 6.9e-150 | | | | |
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| QY | 515 | GGCTACCATTTCTCGAATTTCTTGANGACAACCTTAGAATAATGACATAATGCAATGC | 574 |
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| Db | 213 | TATGATAAGTACTCCAAATGAAAAACAATGCACCCCTTGTCTGTCCAAAGAAATTTGAC | 272 |
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| | mrna | sequence. | | |

REFERENCE

TITLE Generations of ESTs from dormant potato tubers
JOURNAL Unpublished (2001)

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| | 6640.5', mRNA sequence. | |

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| ORGANISM | <i>Solanum tuberosum</i> | |

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 795)

Plum, B., Rothwell, C., Sardan, R., Griffiths, R., Laque, M., De Koeber, D., Andw P., Gower C., Li X -O, Wands-Priest, G. and Pagan S

REFERENCE

AUTHORS

TITLE Generation of ESTs from mature tubers following 1 month storage at 9 degrees celsius, and 95% relative humidity

JOURNAL COMMENT Unpublished (2004)

Contact: Barry Plinn
The Canadian Potato Genome Project - BioAtlantech

FEATURES
source Location/Qualifiers
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/location="1801 James E. Byrnes
921 College Hill Rd, Frederickton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

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conditions. Mature, harvested tubers were stored in the
dark at 9C, 95% relative humidity for 1 month. The tuber
skin was then removed, and RNA was isolated from the
skinless tubers and used for library construction."

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ORIGIN

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|-----------------------|-----------------|-------------------|-----------|-------------|
| Query Match | 54.6%; | Score 616.4; | DB 7; | Length 795; |
| Best Local Similarity | 95.7%; | Pred. No. 9e-150; | | |
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| Db | 331 | TTTTTACTTGCAGACATGGCCCTCATATTTTAAATCTAGTACTGGCCAAATTTTTTGGCCC | 390 |
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 13:22:21 ; Search time 234 Seconds
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7887.693 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 13 | 671.4 | 59.5 | 1158 | 4 | US-09-755-274-38 |
| 14 | 671.4 | 59.5 | 1161 | 4 | US-09-755-630B-285 |
| 15 | 671.4 | 59.5 | 1161 | 4 | US-09-755-274-37 |
| 16 | 652.4 | 57.8 | 1167 | 4 | US-09-755-630B-270 |
| 17 | 652.4 | 57.8 | 1167 | 4 | US-09-755-274-32 |
| 18 | 616 | 54.6 | 1167 | 4 | US-09-755-630B-274 |
| 19 | 616 | 54.6 | 1167 | 4 | US-09-755-274-34 |
| 20 | 608.4 | 53.9 | 1339 | 1 | US-07-936-163-2 |
| 21 | 608 | 53.9 | 1380 | 1 | US-07-936-163-1 |
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| 34 | 50 | 4.4 | 55 | 4 | US-09-755-630B-242 | Sequence 24, App |
| 35 | 50 | 4.4 | 55 | 4 | US-09-755-274-43 | Sequence 43, Appl |
| 36 | 49.4 | 4.4 | 606 | 4 | US-09-248-796A-249 | Sequence 249, App |
| 37 | 47.8 | 4.2 | 51 | 4 | US-09-755-630B-12 | Sequence 12, Appl |
| 38 | 47.8 | 4.2 | 7218 | 1 | US-08-232-463-14 | Sequence 14, Appl |
| 39 | 47.6 | 4.2 | 308 | 4 | US-09-313-294A-3820 | Sequence 3820, Ap |
| 40 | 44.6 | 4.0 | 1141 | 4 | US-09-806-708B-22 | Sequence 22, Appl |
| 41 | 42.8 | 3.8 | 882 | 3 | US-09-276-873-1 | Sequence 1, Appli |
| 42 | 42 | 3.7 | 42 | 4 | US-09-755-630B-243 | Sequence 243, App |
| 43 | 42 | 3.7 | 42 | 4 | US-09-755-274-44 | Sequence 44, Appl |
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ALIGNMENTS

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; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: McHESTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOB7217)
; CURRENT FILING DATE: US/09/755, 630B
; PRIOR APPLICATION NUMBER: 2001-01-05
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
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; OTHER INFORMATION: Synthetic construct
; US-09-755-630B-246

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RESULT 2
 US-09-755-274-20
 ; Sequence 20, Application US/09755274
 ; Patent No. 6657046
 ; GENERAL INFORMATION:
 ; APPLICANT: Alibhai, Murtaza
 ; APPLICANT: Rydel, Timothy
 ; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
 ; FILE REFERENCE: 38-21 (51842)B
 ; CURRENT APPLICATION NUMBER: US/09/755,274
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 20
 ; LENGTH: 1128
 ; TYPE: DNA
 ; ORGANISM: synthetic

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; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1)..(1128)
; OTHER INFORMATION: pMON37402 sequence encoding permuterin protein
US-09-755-274-20

Query Match      100.0%; Score 1128; DB 4; Length 1128;
Best Local Similarity 100.0%; Pred. No. 1,9e-307;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCGAGAAAAGAGAGGCTGAAAGCTTCAATGATATACAAAAAATGCTGTGCTCTCATTTAG 60
Db      1 TCGAGAAAAGAGAGGCTGAAAGCTTCAATGATATACAAAAAATGCTGTGCTCTCATTTAG 60
Qy      61 GCACTGGCACTACTTCAAGAGTTGATPAAACATATACAGCAAAAAGAGGACGTAACCTGGA 120
Db      61 GCACTGGCACTACTTCAAGAGTTGATPAAACATATACAGCAAAAAGAGGACGTAACCTGGA 120
Qy      121 CTGCTGATCACTTGGATGTTATGATTAACAGAAAATGACATGACAGCAAGTTCTTACATGA 180
Db      121 CTGCTGATCACTTGGATGTTATGATTAACAGAAAATGACATGACAGCAAGTTCTTACATGA 180
Qy      181 CTGATTTATTAATCTTCTCACTGCTTTTCAAGCTCTGATTCAAAAAACAATTAACCTGAGG 240
Db      181 CTGATTTATTAATCTTCTCACTGCTTTTCAAGCTCTGATTCAAAAAACAATTAACCTGAGG 240
Qy      241 TTCAAGAAAATGCAATTAACAGGACCAACTATGAAATGATGATGCTTCTGAGGCTPATA 300
Db      241 TTCAAGAAAATGCAATTAACAGGACCAACTATGAAATGATGATGCTTCTGAGGCTPATA 300
Qy      301 TCGAATTTATTAAGTACAGTTGGTGAACCTTATGAAAGAAACCAAGTTTCCGAGACATC 360
Db      301 TCGAATTTATTAAGTACAGTTGGTGAACCTTATGAAAGAAACCAAGTTTCCGAGACATC 360
Qy      361 CTGAAACCTATGAGAGAGCTCTAAGAGGTTTSCAAAATGCTCTGATAGAGAAAGAAC 420
Db      361 CTGAAACCTATGAGAGAGCTCTAAGAGGTTTSCAAAATGCTCTGATAGAGAAAGAAC 420
Qy      421 TCCGAGCAAAACAAGCTTCTTATGACCAAGACAGTTGGAGAAATGGTGACTGTTCTTA 480
Db      421 TCCGAGCAAAACAAGCTTCTTATGACCAAGACAGTTGGAGAAATGGTGACTGTTCTTA 480
Qy      481 GTATTGATGAGAGGTAATGAGAGGATCAATCCGGCTTCACTTCGAAATTTCTTGAG 540
Db      481 GTATTGATGAGAGGTAATGAGAGGATCAATCCGGCTTCACTTCGAAATTTCTTGAG 540
Qy      541 GACAACTTCAGAAATGAGCAATATATGACATGACAGACTTGACAGATTACTTGATGATA 600
Db      541 GACAACTTCAGAAATGAGCAATATATGACATGACAGACTTGACAGATTACTTGATGATA 600
Qy      601 TTGGAGAACAAAGTACAGAGGTTTATGACCTGCTATGATGATGATGATGATGATGATG 660
Db      601 TTGGAGAACAAAGTACAGAGGTTTATGACCTGCTATGATGATGATGATGATGATGATG 660
Qy      661 ATGACCCCTTGCTGCTGCCAAGAAATGATGACCTTTTAACTTGAAACATGAGCCCTCAGA 720
Db      661 ATGACCCCTTGCTGCTGCCAAGAAATGATGACCTTTTAACTTGAAACATGAGCCCTCAGA 720
Qy      721 TTTTAAATCTGATGATCAAAATTTTAAAGCCCAAAATATGATGAAAAATATCTTATGCA 780
Db      721 TTTTAAATCTGATGATCAAAATTTTAAAGCCCAAAATATGATGAAAAATATCTTATGCA 780
Qy      781 TTCTTCAAGAAAACTTGAGAAAATCTGTGTGATCAAGCTTTGACAGAAAGTTGCTATCT 840
Db      781 TTCTTCAAGAAAACTTGAGAAAATCTGTGTGATCAAGCTTTGACAGAAAGTTGCTATCT 840
Qy      841 CAAGCTTTGACATCAAAACAATTAAGCCAGTAATTAATTAATTAATTAATTAATTAATTA 900
Db      841 CAAGCTTTGACATCAAAACAATTAAGCCAGTAATTAATTAATTAATTAATTAATTAATTA 900
Qy      901 CTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Db      901 CTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960

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QY 961 ATTTCTCGCATTAATTGTTACTAATACTAGTAATGAGATGAAATGAGTTCAATC 1020
Db 961 ATTTCTCGCATTAATTGTTACTAATACTAGTAATGAGATGAAATGAGTTCAATC 1020
QY 1021 TTGTTAGTGTGCTGTGTTGTTACTGTTGCTGATCGGCGTTATTAATCAATGAGTTGCAA 1080
Db 1021 TTGTTAGTGTGCTGTGTTGTTACTGTTGCTGATCGGCGTTATTAATCAATGAGTTGCAA 1080
QY 1081 CGAGACTTGCAAAAGAGATCCAGCATTTGCTTCAATTAGTAATGAG 1128
Db 1081 CGAGACTTGCAAAAGAGATCCAGCATTTGCTTCAATTAGTAATGAG 1128

RESULT 3
US-09-755-630B-258
; Sequence 258, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTRAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTERINS
; FILE REFERENCE: 11899.0217, NPUS00 (MORT217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 258
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-755-630B-258

Query Match 91.9%; Score 1036.2; DB 4; Length 1128;
Best Local Similarity 99.2%; Pred. No. 1.4e-281;
Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Db 431 AATTAGAGGATCATTCGGCTACATTCGAAATTCCTTGAAGACAACTTGAGAAAT 490
QY 557 GGAATTAATGAGATGCAAGACTTGCAATTAATTGATGTAATGAGAAACAAGTAC 616
Db 491 GGAATTAATGAGATGCAAGACTTGCAATTAATTGATGTAATGAGAAACAAGTAC 550
QY 617 AGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAACAAATGACCTTTGCTGC 676
Db 551 AGAGGTTTATGACTGCTATGATTAAGTACTCCAAATGAAACAAATGACCTTTGCTGC 610
QY 677 TGGCAAAAGAAATGTATCTTTTAACTTTCGAAACATGCGCTTCGATTTTAACTTAAGTGG 736
Db 611 TGGCAAAAGAAATGTATCTTTTAACTTTCGAAACATGCGCTTCGATTTTAACTTAAGTGG 670
QY 737 TCAATTTTATGCGCCAAATATGATGGAATATCTTATGCAAGTTCTTCAAGAAACT 796
Db 671 TCAATTTTATGCGCCAAATATGATGGAATATCTTATGCAAGTTCTTCAAGAAACT 730
QY 797 TGGAGAAATCTGCTGATCATCACTTTGACAGAGTTGCTCATCAAGCTTTGACATCAA 856
Db 731 TGGAGAAATCTGCTGATCATCACTTTGACAGAGTTGCTCATCAAGCTTTGACATCAA 790
QY 857 AACAAATTAAGCCAGTAATATTCATTAAGTCAAAATTTAGCAAATCTCCAGAAATGATGC 916
Db 791 AACAAATTAAGCCAGTAATATTCATTAAGTCAAAATTTAGCAAATCTCCAGAAATGATGC 850
QY 917 TAAGATGATAGCATATGATTAATTCACAGAGAGCTCCAAATTTTCTCCGACTTA 976
Db 851 TAAGATGATAGCATATGATTAATTCACAGAGAGCTCCAAATTTTCTCCGACTTA 910
QY 977 CTTTGTACTAATAGTATGATGAGATGAATATGAGTCAATCTTTGATGAGTGTGT 1036
Db 911 CTTTGTACTAATAGTATGATGAGATGAATATGAGTCAATCTTTGATGAGTGTGT 970
QY 1037 TGCTACTGTTGCTGATCCGCGTTATTAATTCATTAGGCTGCAACGAGCTTGACAAA 1096
Db 971 TGCTACTGTTGCTGATCCGCGTTATTAATTCATTAGGCTGCAACGAGCTTGACAAA 1030
QY 1097 GGATCCAGCATTTGCTTCAATTAGTAT 1125
Db 1031 GGATCCAGCATTTGCTTCAATTAGTAT 1059

RESULT 4
US-09-755-274-26
; Sequence 26, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtraza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydroxylases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755,274
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1)..(1128)
; OTHER INFORMATION: pMON37407 sequence encoding permuterin protein
US-09-755-274-26

Query Match 91.9%; Score 1036.2; DB 4; Length 1128;
Best Local Similarity 99.2%; Pred. No. 1.4e-281;
Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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| | | | |
|----|------|--|------|
| QY | 137 | GTTAGTATACAGAAAAAGACGTATGACGACAAAGTCTTACATGATGATATTTACCTTC | 196 |
| Db | 71 | GTTAGTATACAGAAAAAGACGTATGACGACAAAGTCTTACATGATGATATTTACCTTC | 130 |
| QY | 197 | TACTGCTTTTCAAGCTTTGATTCAAAAACAATTCTCAAGGTTCAAGAAAAATGCATT | 256 |
| Db | 131 | TACTGCTTTTCAAGCTTTGATTCAAAAACAATTCTCAAGGTTCAAGAAAAATGCATT | 190 |
| QY | 257 | AACAGGCAACACTACTGAAATGAGTATGAGCTTCGAGGCTTAATGAAATTAATGATCA | 316 |
| Db | 191 | AACAGGCAACACTACTGAAATGAGTATGAGCTTCGAGGCTTAATGAAATTAATGATCA | 250 |
| QY | 317 | AGTTGGTGAATACTTATGAGAAACAGAGTTCCGAAACACATCCTGAAACCTATGAGCA | 376 |
| Db | 251 | AGTTGGTGAATACTTATGAGAAACAGAGTTCCGAAACACATCCTGAAACCTATGAGCA | 310 |
| QY | 377 | AGCTCTAAGAAGTTTGCAAAATTCCTCTGTATGAGAAAGAACTCCGAGCAACAAAGC | 436 |
| Db | 311 | AGCTCTAAGAAGTTTGCAAAATTCCTCTGTATGAGAAAGAACTCCGATCAAAACAAAGC | 370 |
| QY | 437 | TTCTTATGACACAGGACGTTGGGGAATAAGTGACTGTCTGTAATGATGAGAGTG | 496 |
| Db | 371 | TTCTTATGACACAGGACGTTGGGGAATAAGTGACTGTCTGTAATGATGAGAGTG | 430 |
| QY | 497 | AATTAGAGGATCAATCCGGCTACCATTCGCAATTTCTGAGGACAACTTCAGAAAT | 556 |
| Db | 431 | AATTAGAGGATCAATCCGGCTACCATTCGCAATTTCTGAGGACAACTTCAGAAAT | 490 |
| QY | 557 | GGACAAATATGCAATGCAAGTGCAGACTTCGAGATTACTTTGATGTAATGGAGGAACAATAC | 616 |
| Db | 491 | GGACAAATATGCAAGTGCAGACTTCGAGATTACTTTGATGTAATGGAGGAACAATAC | 550 |
| QY | 617 | AGGAGGTTTATGTAAGTGTATGATPAAAGTATCCAAATGAAAACAATGACCCCTTGCTGC | 676 |
| Db | 551 | AGGAGGTTTATGTAAGTGTATGATPAAAGTATCCAAATGAAAACAATGACCCCTTGCTGC | 610 |
| QY | 677 | TGCCAAGAAATGTACCTTTTACCTTGCAACATGAGCCCTCAGATTTTAAATCCTAAGTG | 736 |
| Db | 611 | TGCCAAGAAATGTACCTTTTACCTTGCAACATGAGCCCTCAGATTTTAAATCCTAAGTG | 670 |
| QY | 737 | TCAATTTTACGCCCAAAATATGATGAGAAATATCTTATGCAAGTCTTCGAAGAAAACT | 796 |
| Db | 671 | TCAATTTTACGCCCAAAATATGATGAGAAATATCTTATGCAAGTCTTCGAAGAAAACT | 730 |
| QY | 797 | TGAGAAACTGTGTGCATCAAGCTTTGACAGAAAGTTGTCAATCTCAAGCTTTGACATCA | 856 |
| Db | 731 | TGAGAAACTGTGTGCATCAAGCTTTGACAGAAAGTTGTCAATCTCAAGCTTTGACATCA | 790 |
| QY | 857 | AACAAATAGCCAGTAATATTCCTAAGTCAAAATTTAGCAAACTCTCGAAGATTTGATGC | 916 |
| Db | 791 | AACAAATAGCCAGTAATATTCCTAAGTCAAAATTTAGCAAACTCTCGAAGATTTGATGC | 850 |
| QY | 917 | TAAATGATGACAAATTAATTTCCAGACGACAGCTCCAAATATTTTCTCCGCAATTA | 976 |
| Db | 851 | TAAATGATGACAAATTAATTTCCAGACGACAGCTCCAAATATTTTCTCCGCAATTA | 910 |
| QY | 977 | CTTTGTTACTATACTAGTAATGAGAGAAATATAGTTTCAATCTTGTTAGTGTGTGT | 1038 |
| Db | 911 | CTTTGTTACTATACTAGTAATGAGAGAAATATAGTTTCAATCTTGTTAGTGTGTGT | 970 |
| QY | 1037 | TGCTACTGTGCTGATCCGGGCTTATTAATCCATTAGCGTTGCAAGCACTTGCAAAA | 1096 |
| Db | 971 | TGCTACTGTGCTGATCCGGGCTTATTAATCCATTAGCGTTGCAAGCACTTGCAAAA | 1030 |
| QY | 1097 | GGATCCAGCATTTGCTTCAATTAGGTAAAT | 1125 |
| Db | 1031 | GGATCCAGCATTTGCTTCAATTAGGTAAAT | 1059 |

```

? Patent No.6639054
? GENERAL INFORMATION:
? APPLICANT: ALIHAJI, MURTAZA F.
? APPLICANT: ASTWOOD, JAMES D.
? APPLICANT: SAMPERSON, HUGH A.
? APPLICANT: MCHESTER, CHARLES A.
? TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
? FILE REFERENCE: 11899, 0217.NPUS00 (MOB217)
? CURRENT APPLICATION NUMBER: US/09/755,630B
? CURRENT FILING DATE: 2001-01-05
? PRIOR APPLICATION NUMBER: US 60/174,669
? PRIOR FILING DATE: 2000-01-06
? NUMBER OF SEQ ID NOS: 295
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 250
? LENGTH: 1128
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic construct
? US-09-755-630B-250

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| | | | | |
|-----------------------|-----------------|---------------------|-----------|--------------|
| Query Match | 85.4%; | Score 963.4; | DB 4; | Length 1128; |
| Best Local Similarity | 99.9%; | Pred. No. 4.3e-261; | | |
| Matches 964; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |

| | | | | | |
|----|-----|-------------|--|------------------|-----|
| OY | 24 | TCATTGAATTA | CAAAAAAATGCTGTGGCTCTCATTTAGGCACTGGCACTACTTCAGAGTTT | 83 | |
| Db | 159 | TCATTGAATTA | CAAAAAAATGCTGTGGCTCTCATTTAGGCACTGGCACTACTTCAGAGTTT | 218 | |
| OY | 84 | GATAAAA | CATATACGCAAAAAGGCGAGCTACCTGGACTGCTGTACATTTGATGTAGTT | 143 | |
| Db | 219 | GATAAAA | CATATACGCAAAAAGGCGAGCTACCTGGACTGCTGTACATTTGATGTAGTT | 278 | |
| OY | 144 | ATACGAAAAA | AGACGAGTGTCTTACATGACGTGATTTATTA | CTTTCTTACTGTCT | 203 |
| Db | 279 | ATACGAAAAA | AGACGAGTGTCTTACATGAGTGTCTTACATGAGTGTATTTACTCTTCTTACTGTCT | 338 | |
| OY | 204 | TTTCAAGCTCT | TGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAAATGCAATTAA | CAGGC | 263 |
| Db | 339 | TTTCAAGCTCT | TGATTCAAAAAACAATTACCTCAGGGTTCAAGAAAAATGCAATTAA | CAGGC | 398 |
| OY | 264 | ACAACTACTG | AAATGATGATGCTTCTTGAGGCTTAATAGAAATTATTA | AGTCAAGTTGCT | 323 |
| Db | 399 | ACAACTACTG | AAATGATGATGCTTCTTGAGGCTTAATAGAAATTATTA | AGTCAAGTTGCT | 458 |
| OY | 324 | GAAAACTA | TTGAAGAAAAACAGTTTCCGAAACAATCCTGAAACCTATGAGGAAGCTCTA | 383 | |
| Db | 459 | GAAAACTA | TTGAAGAAAAACAGTTTCCGAAACAATCCTGAAACCTATGAGGAAGCTCTA | 518 | |
| OY | 384 | AAGAGCTTTG | CAAAATTTGCTCTCTTGATAGGAAGAACTCCGAGCAACAAGCTTTCTAT | 443 | |
| Db | 519 | AAGAGCTTTG | CAAAATTTGCTCTCTTGATAGGAAGAACTCCGAGCAACAAGCTTTCTAT | 578 | |
| OY | 444 | GGACGAGG | ACAGTTGGGAGAAATGCTGACTCTTCTTATGATTTGATGAGAGTGTGAAATTAGA | 503 | |
| Db | 579 | GGACGAGG | ACAGTTGGGAGAAATGCTGACTCTTCTTATGATTTGATGAGAGTGTGAAATTAGA | 638 | |
| OY | 504 | GGGATTCAT | TCGGGCTACCATTTCTGAAATTTCTTGAAGCAACA | CTTCAGGAATGACAAT | 563 |
| Db | 639 | GGGATTCAT | TCGGGCTACCATTTCTGAAATTTCTTGAAGCAACA | CTTCAGGAATGACAAT | 698 |
| OY | 564 | AATGACAGT | CAACAACCTTGACAGATTTACTTTGATGTAAATGGAAGGAAACAATGACAGAGGT | 623 | |
| Db | 699 | AATGACAGT | CAACAACCTTGACAGATTTACTTTGATGTAAATGGAAGGAAACAATGACAGAGGT | 758 | |
| OY | 624 | TTATTTGA | CTGCTGATGATAGTACTTCCAATGAAAAACAATGCAACCTTTGCTGTGCAAA | 683 | |
| Db | 759 | TTATTTGA | CTGCTGATGATAGTACTTCCAATGAAAAACAATGCAACCTTTGCTGTGCAAA | 818 | |
| OY | 684 | GAAATTTGA | CTTTTATCTTGAAACATGCGCCTCAGATTTTATTAATCCTAGTGTCAAAAT | 743 | |
| Db | 819 | GAAATTTGA | CTTTTATCTTGAAACATGCGCCTCAGATTTTATTAATCCTAGTGTCAAAAT | 878 | |

QY 744 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTCTTCAAGAAAACTTGGAGAA 803
Db 879 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTCTTCAAGAAAACTTGGAGAA 938
QY 804 ACTGCTGTCATCAAGCTTTGACAGAAAGTGTCTCTCAAGCTTTGACATCAAAACAAT 863
Db 939 ACTGCTGTCATCAAGCTTTGACAGAAAGTGTCTCTCAAGCTTTGACATCAAAACAAT 998
QY 864 AAGCCAGTAATATCTAGTCAAAATTTGCAAACTCTCAGAAATGAGTGAAGATG 923
Db 999 AAGCCAGTAATATCTAGTCAAAATTTGCAAACTCTCAGAAATGAGTGAAGATG 1058
QY 924 TATGACATAAGTATTTCCACAGCAGAGCTCCAAATATTTTCTCCGCAATTAATTGTT 983
Db 1059 TATGACATAAGTATTTCCACAGCAGAGCTCCAAATATTTTCTCCGCAATTAATTGTT 1118
QY 984 ACTAA 988
Db 1119 ACTTA 1123

RESULT 6
US-09-755-274-22
; Sequence 22, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755,274
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1)..(1128)
; OTHER INFORMATION: pMON37405 sequence encoding permutein protein
; US-09-755-274-22

Query Match 85.4%; Score 963.4; DB 4; Length 1128;
Best Local Similarity 99.9%; Pred. No. 4.3e-261;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 TCATTGATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCAGTCTTCAAGTTT 83
Db 159 TCATTGATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCAGTCTTCAAGTTT 218
QY 84 GATATAACATATATACAGAAAAAGGAGCAGTACCTGAGCTGCTGATCATTTGATTTAGTT 143
Db 219 GATATAACATATATACAGAAAAAGGAGCAGTACCTGAGCTGCTGATCATTTGATTTAGTT 278
QY 144 ATACAGAAATGACTGATGACAGAGTTCTTACATGATGATTTATTAACCTTTTACTGCT 203
Db 279 ATACAGAAATGACTGATGACAGAGTTCTTACATGATGATTTATTAACCTTTTACTGCT 338
QY 204 TTTCAGGCTCTGATTTCAAAAAACAATTACCTGAGGTTCAAGAAATGATTAACAGGC 263
Db 339 TTTCAGGCTCTGATTTCAAAAAACAATTACCTGAGGTTCAAGAAATGATTAACAGGC 398
QY 264 ACAACTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTTATTAACAAGTTGT 323
Db 399 ACAACTACTGAAATGATGATGCTTCTGAGGCTAATATGAAATTTATTAACAAGTTGT 458
QY 324 GAAATCTTATTTGAAGAAACAGTTTCCGAGAGCAATCTTGAACCTTATGAGAAAGCTCTA 383
Db 459 GAAATCTTATTTGAAGAAACAGTTTCCGAGAGCAATCTTGAACCTTATGAGAAAGCTCTA 518

QY 384 AAGAGTTTGCAAAATTTCTCTGATGAGAGAACTCCGAGCAAAACAAGCTTCTTAT 443
Db 519 AAGAGTTTGCAAAATTTCTCTGATGAGAGAACTCCGAGCAAAACAAGCTTCTTAT 578
QY 444 GGACCCAGAGAGTTGGAGAAATGATGATCTGTTCTTGTATGATGAGAGTGAATTTGA 503
Db 579 GGACCCAGAGAGTTGGAGAAATGATGATCTGTTCTTGTATGATGAGAGTGAATTTGA 638
QY 504 GGGATCATTCGGGCTACATTTCTGAAATTTCTTGAAGACAATCTTCAAGAAATGAGCAAT 563
Db 639 GGGATCATTCGGGCTACATTTCTGAAATTTCTTGAAGACAATCTTCAAGAAATGAGCAAT 698
QY 564 AATGACAGTCAAGACTTGCAGATTTACTTGTATGATTTGAGAGAACAGTACAGAGGT 623
Db 699 AATGACAGTCAAGACTTGCAGATTTACTTGTATGATTTGAGAGAACAGTACAGAGGT 758
QY 624 TTATGACTGCTATGATTAAGTACTCCAAATGAAACATGACCTTTGCTGCTCCAA 683
Db 759 TTATGACTGCTATGATTAAGTACTCCAAATGAAACATGACCTTTGCTGCTCCAA 818
QY 684 GAAATGTACTTTTACTTGAACATGGCCCTCAGATTTTAACTCAGTGTCAAT 743
Db 819 GAAATGTACTTTTACTTGAACATGGCCCTCAGATTTTAACTCAGTGTCAAT 878
QY 744 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTCTTCAAGAAAACTTGGAGAA 803
Db 879 TTAGGCCCAAAATATGATGAAAAATATCTTATGCAAGTCTTCAAGAAAACTTGGAGAA 938
QY 804 ACTGCTGTCATCAAGCTTTGACAGAAAGTGTCTCTCAAGCTTTGACATCAAAACAAT 863
Db 939 ACTGCTGTCATCAAGCTTTGACAGAAAGTGTCTCTCAAGCTTTGACATCAAAACAAT 998
QY 864 AAGCCAGTAATATCTAGTCAAAATTTGCAAACTCTCAGAAATGAGTGAAGATG 923
Db 999 AAGCCAGTAATATCTAGTCAAAATTTGCAAACTCTCAGAAATGAGTGAAGATG 1058
QY 924 TATGACATAAGTATTTCCACAGCAGAGCTCCAAATATTTTCTCCGCAATTAATTGTT 983
Db 1059 TATGACATAAGTATTTCCACAGCAGAGCTCCAAATATTTTCTCCGCAATTAATTGTT 1118
QY 984 ACTAA 988
Db 1119 ACTTA 1123

RESULT 7
US-09-755-630B-254
; Sequence 254, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 254
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-09-755-630B-254

Query Match 80.6%; Score 909; DB 4; Length 1128;
Best Local Similarity 100.0%; Pred. No. 9e-246;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 TATATTGATGAGGAGTGAATTAAGAGATCATTCGGCTTACCAATTCGAAATTTCTTGA 313
 QY 539 AGGACAACTTCAGAAATGAGCAATATATGAGATGCAAGACTTGCAGATTACTTGTATGT 598
 Db 314 AGGACAACTTCAGAAATGAGCAATATATGAGATGCAAGACTTGCAGATTACTTGTATGT 373
 QY 599 AATTGAGCAAGCAATGACAGAGGTTTATGACTGCTATGATTAATCTCCAAATGAAA 658
 Db 374 AATTGAGCAAGCAATGACAGAGGTTTATGACTGCTATGATTAATCTCCAAATGAAA 433
 QY 659 CAATGACCCCTTGTGCTGCTGCAAGAAATGTACCTTTTACTTGAACATGAGCCCTCA 718
 Db 434 CAATGACCCCTTGTGCTGCTGCAAGAAATGTACCTTTTACTTGAACATGAGCCCTCA 493
 QY 719 GATTTTAACTCTAGTGTCAAAATTTAGGCCCAAAATATGATGAAATATCTTATGCA 778
 Db 494 GATTTTAACTCTAGTGTCAAAATTTAGGCCCAAAATATGATGAAATATCTTATGCA 553
 QY 779 AGTTCTTCAAGAAAATCTGAGAAATCTGCTGCTCATCAAGCTTTGACAGAGTTGTCT 838
 Db 554 AGTTCTTCAAGAAAATCTGAGAAATCTGCTGCTCATCAAGCTTTGACAGAGTTGTCT 613
 QY 839 CTCAGCTTTGACATCAAAACAATAAGCCAGTAAATATGACTTAAGTCAATTTAGCAAA 898
 Db 614 CTCAGCTTTGACATCAAAACAATAAGCCAGTAAATATGACTTAAGTCAATTTAGCAAA 673
 QY 899 CTCCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
 Db 674 CTCCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 733
 QY 959 ATATTTTCTCCGCAATTAATTTTACTTAATTAATTAATTAATTAATTAATTAATTAAT 1018
 Db 734 ATATTTTCTCCGCAATTAATTTTACTTAATTAATTAATTAATTAATTAATTAATTAAT 793
 QY 1019 TCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1078
 Db 794 TCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 853
 QY 1079 AACGAGACTTGCACAAAAGAGATCCAGATTTGCTTCATTAAGTAAAT 1125
 Db 854 AACGAGACTTGCACAAAAGAGATCCAGATTTGCTTCATTAAGTAAAT 900

RESULT 11
 US-09-755-630B-5
 ; Sequence 5, Application US/09755630B
 ; Patent No. 6639054
 ; GENERAL INFORMATION:
 ; APPLICANT: ALIBHAI, MURTAZA F.
 ; APPLICANT: ASTWOOD, JAMES D.
 ; APPLICANT: SAMPSON, HUGH A.
 ; APPLICANT: MCHESTER, CHARLES A.
 ; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTAINS
 ; CURRENT APPLICATION NUMBER: US/09/755,630B
 ; PRIOR FILING DATE: 2001-01-05
 ; PRIOR FILING DATE: 2000-01-06
 ; NUMBER OF SEQ ID NOS: 295
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 1138
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct
 US-09-755-630B-5

Query Match 59.6%; Score 672.2; DB 4; Length 1138;
 Best local Similarity 99.6%; Pred. No. 4,3e-179;
 Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 449 AGGACAGTTGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
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 Db 85 CATTCCGGCTACCATTTCTGAAATTTCTTGAAGACAACTTCAGAAATGAGCAATTAATGC 144
 QY 569 AGATGCAAGCTTGCAGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 628
 Db 145 AGATGCAAGCTTGCAGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 204
 QY 629 GACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
 Db 205 GACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 264
 QY 689 TGATCTTTTAACTTGAACATGAGCCCTGAGATTTTAAATCTTGAAGTCAATTTTAAAG 748
 Db 265 TGATCTTTTAACTTGAACATGAGCCCTGAGATTTTAAATCTTGAAGTCAATTTTAAAG 324
 QY 749 CCCAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAATCTGAGAAAATCTCG 808
 Db 325 CCCAAATATGATGAAATATCTTATGCAAGTTCTTCAAGAAAATCTGAGAAAATCTCG 384
 QY 809 TGTGCAATCAAGCTTTGACAGAGTTGTCTCATCTCAAGCTTTGACATCAAAACAATAAGCC 868
 Db 385 TGTGCAATCAAGCTTTGACAGAGTTGTCTCATCTCAAGCTTTGACATCAAAACAATAAGCC 444
 QY 869 AGTAATATTCATCAATGATCAATTTTAACTTCAGAAATCTGAGAAATGATGATGATGAT 928
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RESULT 12
 US-09-755-630B-1
 ; Sequence 1, Application US/09755630B
 ; Patent No. 6639054
 ; GENERAL INFORMATION:
 ; APPLICANT: ALIBHAI, MURTAZA F.
 ; APPLICANT: ASTWOOD, JAMES D.
 ; APPLICANT: SAMPSON, HUGH A.
 ; APPLICANT: MCHESTER, CHARLES A.
 ; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTAINS
 ; CURRENT APPLICATION NUMBER: US/09/755,630B
 ; PRIOR FILING DATE: 2001-01-05
 ; PRIOR FILING DATE: 2000-01-06
 ; NUMBER OF SEQ ID NOS: 295
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1158
 ; TYPE: DNA
 ; ORGANISM: Solanum tuberosum
 US-09-755-630B-1

Query Match 59.5%; Score 671.4; DB 4; Length 1158;

LENGTH: 1161
TYPE: DNA
ORGANISM: Solanum tuberosum
US-09-755-630B-285

Query Match 59.5%; Score 671.4; DB 4; Length 1161;
Best Local Similarity 99.9%; Pred. No. 7.4e-179;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 130 CCGGCTACCACTTCGAAATTTCTTGAAGACAATTCAGAAATGACAAATATGAGAT 189
QY 573 GCAAGCTTGCAAGTATCTTGTATGATGAGAGAAACAGTACAGAGGTTATGACT 632
DB 190 GCAAGCTTGCAAGTATCTTGTATGATGAGAGAAACAGTACAGAGGTTATGACT 249
QY 633 GCTATGATAGTACTCCAAATGAAAACATCGACCTTGTCTGCGCAAAAGATTTG 692
DB 250 GCTATGATAGTACTCCAAATGAAAACATCGACCTTGTCTGCGCAAAAGATTTG 309
QY 693 CCTTTTACTTGCAACATGCGCCCTCAGATTTTAACTAGTGTCAAAATTTAGCCCA 752
DB 310 CCTTTTACTTGCAACATGCGCCCTCAGATTTTAACTAGTGTCAAAATTTAGCCCA 369
QY 753 AAATATGATGAAAATATCTTATGCAAGTCTTCAAGAAAATCTGAGAACTCGTGTG 812
DB 370 AAATATGATGAAAATATCTTATGCAAGTCTTCAAGAAAATCTGAGAACTCGTGTG 429
QY 813 CATCAAGCTTTGACAGAAAGTGTCTATCTCAAGCTTTGACATCAAAACAAATAGCCAGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTGTCTATCTCAAGCTTTGACATCAAAACAAATAGCCAGTA 489
QY 873 ATATTGACTAGTCAAAATTTAGCAAACTCTCCAGAAATGAGTCTAAGATGATGACATA 932
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QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTAAT 742
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RESULT 15

US-09-755-274-37
Sequence 37, Application US/09755274
Patent No. 6657046
GENERAL INFORMATION:
APPLICANT: Pydel, Murteza
TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydroxylases
FILE REFERENCE: 38-21 (51842)B
CURRENT APPLICATION NUMBER: US/09/755,274
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.0
SEQ ID NO 37
LENGTH: 1161

TYPE: DNA
ORGANISM: Solanum cardiophyllum
FEATURE:
NAME/KEY: exon
LOCATION: (1)..(1161)
OTHER INFORMATION: patatin homolog Pat17 nucleic acid and amino acid translation
US-09-755-274-37

Query Match 59.5%; Score 671.4; DB 4; Length 1161;
Best Local Similarity 99.9%; Pred. No. 7.4e-179;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 70 CAGTTGGAGAAATGTGACTGTTCTTAGTATGATGAGAGTGAATAGAGGATCAT 129
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DB 130 CCGGCTACCACTTCGAAATTTCTTGAAGACAATTCAGAAATGACAAATATGAGAT 189
QY 573 GCAAGCTTGCAAGTATCTTGTATGATGAGAGAAACAGTACAGAGGTTATGACT 632
DB 190 GCAAGCTTGCAAGTATCTTGTATGATGAGAGAAACAGTACAGAGGTTATGACT 249
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DB 250 GCTATGATAGTACTCCAAATGAAAACATCGACCTTGTCTGCGCAAAAGATTTG 309
QY 693 CCTTTTACTTGCAACATGCGCCCTCAGATTTTAACTAGTGTCAAAATTTAGCCCA 752
DB 310 CCTTTTACTTGCAACATGCGCCCTCAGATTTTAACTAGTGTCAAAATTTAGCCCA 369
QY 753 AAATATGATGAAAATATCTTATGCAAGTCTTCAAGAAAATCTGAGAACTCGTGTG 812
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QY 813 CATCAAGCTTTGACAGAAAGTGTCTATCTCAAGCTTTGACATCAAAACAAATAGCCAGTA 872
DB 430 CATCAAGCTTTGACAGAAAGTGTCTATCTCAAGCTTTGACATCAAAACAAATAGCCAGTA 489
QY 873 ATATTGACTAGTCAAAATTTAGCAAACTCTCCAGAAATGAGTCTAAGATGATGACATA 932
DB 490 ATATTGACTAGTCAAAATTTAGCAAACTCTCCAGAAATGAGTCTAAGATGATGACATA 549
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QY 993 AGTAATGAGATGATATGATGATCAATCTTGTGATGATGCTGTGCTACTGTTGCTGAT 1052
DB 610 AGTAATGAGATGATATGATGATCAATCTTGTGATGATGCTGTGCTACTGTTGCTGAT 669
QY 1053 CCGGCGTTATTTATCCATTAGCGTTGCAACGAGACTTGCAAAAAGATCCAGATTTGCT 1112
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QY 1113 TCAATTAGGTAAT 1125
DB 730 TCAATTAGGTAAT 742
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Job time : 237 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 15:10:06 ; Search time 686 Seconds
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9964.554 Million cell updates/sec

Title: US-10-658-180-246

Perfect score: 1128
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Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|--------|-------------|--------|----|--------------------------------------|
| 1 | 1128 | 100.0 | 1128 | 10 | US-09-755-630A-246 Sequence 246, App |
| 2 | 1128 | 100.0 | 1128 | 18 | US-10-658-180-246 Sequence 246, App |
| 3 | 1128 | 100.0 | 1128 | 18 | US-10-682-011-20 Sequence 20, App |
| 4 | 1036.2 | 91.9 | 1128 | 10 | US-09-755-630A-258 Sequence 258, App |
| 5 | 1036.2 | 91.9 | 1128 | 18 | US-10-658-180-258 Sequence 258, App |
| 6 | 1036.2 | 91.9 | 1128 | 18 | US-10-682-011-26 Sequence 26, App |
| 7 | 963.4 | 85.4 | 1128 | 10 | US-09-755-630A-250 Sequence 250, App |
| 8 | 963.4 | 85.4 | 1128 | 18 | US-10-658-180-250 Sequence 250, App |
| 9 | 963.4 | 85.4 | 1128 | 18 | US-10-682-011-22 Sequence 22, App |
| 10 | 909 | 80.6 | 1128 | 10 | US-09-755-630A-254 Sequence 254, App |
| 11 | 909 | 80.6 | 1128 | 18 | US-10-658-180-254 Sequence 254, App |

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| 12 | 909 | 80.6 | 1128 | 18 | US-10-682-011-24 Sequence 24, App |
| 13 | 879 | 77.9 | 1128 | 10 | US-09-755-630A-262 Sequence 262, App |
| 14 | 879 | 77.9 | 1128 | 18 | US-10-658-180-262 Sequence 262, App |
| 15 | 879 | 77.9 | 1128 | 18 | US-10-682-011-28 Sequence 28, App |
| 16 | 672.2 | 59.6 | 1128 | 10 | US-09-755-630A-5 Sequence 5, App |
| 17 | 672.2 | 59.6 | 1128 | 18 | US-10-658-180-5 Sequence 5, App |
| 18 | 671.4 | 59.5 | 1128 | 10 | US-09-755-630A-1 Sequence 1, App |
| 19 | 671.4 | 59.5 | 1128 | 18 | US-10-658-180-1 Sequence 1, App |
| 20 | 671.4 | 59.5 | 1128 | 18 | US-10-682-011-38 Sequence 38, App |
| 21 | 671.4 | 59.5 | 1128 | 10 | US-09-755-630A-285 Sequence 285, App |
| 22 | 671.4 | 59.5 | 1128 | 18 | US-10-658-180-285 Sequence 285, App |
| 23 | 671.4 | 59.5 | 1128 | 10 | US-10-682-011-37 Sequence 37, App |
| 24 | 652.4 | 57.8 | 1128 | 18 | US-09-755-630A-270 Sequence 270, App |
| 25 | 652.4 | 57.8 | 1128 | 18 | US-10-658-180-270 Sequence 270, App |
| 26 | 652.4 | 57.8 | 1128 | 18 | US-10-682-011-32 Sequence 32, App |
| 27 | 616 | 54.6 | 1128 | 10 | US-09-755-630A-274 Sequence 274, App |
| 28 | 616 | 54.6 | 1128 | 18 | US-10-658-180-274 Sequence 274, App |
| 29 | 616 | 54.6 | 1128 | 18 | US-10-682-011-34 Sequence 34, App |
| 30 | 390.6 | 34.6 | 1128 | 10 | US-09-755-630A-264 Sequence 264, App |
| 31 | 390.6 | 34.6 | 1128 | 18 | US-10-658-180-264 Sequence 264, App |
| 32 | 390.6 | 34.6 | 1128 | 18 | US-10-682-011-30 Sequence 30, App |
| 33 | 194 | 17.2 | 1009 | 17 | US-10-424-599-466 Sequence 466, App |
| 34 | 185.2 | 16.4 | 276 | 17 | US-10-417-280A-50 Sequence 50, App |
| 35 | 149.2 | 13.2 | 1245 | 9 | US-09-938-842A-2546 Sequence 2546, App |
| 36 | 149.2 | 13.2 | 1245 | 11 | US-09-938-842A-2546 Sequence 2546, App |
| 37 | 143 | 12.7 | 1164 | 18 | US-10-437-963-75340 Sequence 75340, App |
| 38 | 140.8 | 12.5 | 1170 | 14 | US-10-034-937-3 Sequence 3, App |
| 39 | 140.8 | 12.5 | 1170 | 14 | US-10-034-937-11 Sequence 11, App |
| 40 | 139.6 | 12.4 | 1170 | 14 | US-10-034-937-15 Sequence 15, App |
| 41 | 139.6 | 12.4 | 1170 | 14 | US-10-034-937-19 Sequence 19, App |
| 42 | 139.2 | 12.3 | 1161 | 14 | US-10-034-937-1 Sequence 1, App |
| 43 | 139.2 | 12.3 | 1170 | 14 | US-10-034-937-25 Sequence 25, App |
| 44 | 139.2 | 12.3 | 1170 | 14 | US-10-034-937-27 Sequence 27, App |
| 45 | 139.2 | 12.3 | 1170 | 14 | US-10-034-937-29 Sequence 29, App |

ALIGNMENTS

RESULT 1
US-09-755-630A-246
; Sequence 246, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHIRTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTAINS
; FILE REFERENCE: 11899.0217.NPUS00 (MORT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-755-630A-246

Query Match 100.0%; Score 1128; DB 10; Length 1128;
Best Local Similarity 100.0%; Pred. No. 2,8e-276;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TCGAGAAAAGAGAGGCTGAGCTTCATGTGATATACAAAAGCTTCTCTCTCTAG 60
QY 61 GCACTGCACTACTCTAGAGTTGATTAACATATACAGCAAGAGGACGACTACTGGA 120

| | | | |
|----|------|---|------|
| Db | 61 | GCACCTGGACACACCTTTCAGAGCTTTGATTAACACATATACGACCAAAAGGACACCTACCTGGA | 120 |
| Qy | 121 | CTGCTGTACATTGGATGTTAGTTATATACGAAAATGACTGATGCAGCAAGTTCTTACATGA | 180 |
| Db | 121 | CTGCTGTACATTGGATGTTAGTTATATACGAAAATGACTGATGCAGCAAGTTCTTACATGA | 180 |
| Qy | 181 | CTGATATATACCTTTCTATCTGCTTTTCAAGCTCTTGATTTCAAAAAAACAATTACCTCAGGG | 240 |
| Db | 181 | CTGATATATACCTTTCTATCTGCTTTTCAAGCTCTTGATTTCAAAAAAACAATTACCTCAGGG | 240 |
| Qy | 241 | TTCAAGAAAATGCAATTAAACAGGCAACACTACTGAAATGATATGCTTCTGAGGCTAATA | 300 |
| Db | 241 | TTCAAGAAAATGCAATTAAACAGGCAACACTACTGAAATGATATGCTTCTGAGGCTAATA | 300 |
| Qy | 301 | TGGAATTATAGTACAAAGTTGCTGAAAACCTTATGGAAGAAAACAAGTTTCCGAAGCAATC | 360 |
| Db | 301 | TGGAATTATAGTACAAAGTTGCTGAAAACCTTATGGAAGAAAACAAGTTTCCGAAGCAATC | 360 |
| Qy | 361 | CTGAAACCTATAGAGAAAGCTCTAAAGAGTTTGAAAATTTGCTCTCTGATATGGAAGAAAC | 420 |
| Db | 361 | CTGAAACCTATAGAGAAAGCTCTAAAGAGTTTGAAAATTTGCTCTCTGATATGGAAGAAAC | 420 |
| Qy | 421 | TCCGAGCAAAACAAGCTTCTATGGAACAGACAGATTGGGAGAAAATGATGACTGTTCTTA | 480 |
| Db | 421 | TCCGAGCAAAACAAGCTTCTATGGAACAGACAGATTGGGAGAAAATGATGACTGTTCTTA | 480 |
| Qy | 481 | GTAATTGATGAGGTGGAATTAGAGGATCAATTCGGGCTTACCAATTCGAAATTTCTTGAG | 540 |
| Db | 481 | GTAATTGATGAGGTGGAATTAGAGGATCAATTCGGGCTTACCAATTCGAAATTTCTTGAG | 540 |
| Qy | 541 | GACAACTTCAGAAAATGGAACAAATATAGAGATGCAAGACTTGCGAGATTACTTTGATATGAA | 600 |
| Db | 541 | GACAACTTCAGAAAATGGAACAAATATAGAGATGCAAGACTTGCGAGATTACTTTGATATGAA | 600 |
| Qy | 601 | TTGAGAGAAACAAGTACAGAGGTTTATTTGACTGCTATGATATAGTACTCCAATGAAAACA | 660 |
| Db | 601 | TTGAGAGAAACAAGTACAGAGGTTTATTTGACTGCTATGATATAGTACTCCAATGAAAACA | 660 |
| Qy | 661 | ATCGAACCTTTGCTGCTGCCAAAAGAAATTTGACCTTTTACTTGGAAATGAGCCCTCAGA | 720 |
| Db | 661 | ATCGAACCTTTGCTGCTGCCAAAAGAAATTTGACCTTTTACTTGGAAATGAGCCCTCAGA | 720 |
| Qy | 721 | TTTTTAAATCCATGAGTGTCAAAATTTTAGGCCCAAAAATGATGAGAAAATATCTTATGCAAG | 780 |
| Db | 721 | TTTTTAAATCCATGAGTGTCAAAATTTTAGGCCCAAAAATGATGAGAAAATATCTTATGCAAG | 780 |
| Qy | 781 | TTCTTCAAGAAAAAATTGGAGAAACTCGTGTGCATCAAGCTTTTGCAGAAATTTGTCTACT | 840 |
| Db | 781 | TTCTTCAAGAAAAAATTGGAGAAACTCGTGTGCATCAAGCTTTTGCAGAAATTTGTCTACT | 840 |
| Qy | 841 | CAAGCTTTGACATCAAAAACAATAAGCAGATATATTCATATAGTCAAAATTTAGCAAACT | 900 |
| Db | 841 | CAAGCTTTGACATCAAAAACAATAAGCAGATATATTCATATAGTCAAAATTTAGCAAACT | 900 |
| Qy | 901 | CTCCAGATTTGGATGCTAGATATGATATGACATTAATTTCCACAGCAGACACTCCAAAT | 960 |
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| Qy | 961 | ATTTTTCCTCCGCACTTACTTTGTACTAATATCTAGTAATGAGATGAAATATATGAGTTCAATC | 1020 |
| Db | 961 | ATTTTTCCTCCGCACTTACTTTGTACTAATATCTAGTAATGAGATGAAATATATGAGTTCAATC | 1020 |
| Qy | 1021 | TTGTTGATGCTGCTGTTGCTTACTGTGCTGATCCGGCGTTATATATCATATGACGTTGCAA | 1080 |
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| Qy | 1081 | CGAGACTTGCACAAAAGATCCAGATTTTGTCTCAATTAGATGAAG 1128 | |
| Db | 1081 | CGAGACTTGCACAAAAGATCCAGATTTTGTCTCAATTAGATGAAG 1128 | |

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US-10-658-180-246
; Sequence 246, Application US/10658180
; Publication No. US20040216187A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: McHWERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTATIONS
; FILE REFERENCE: 11899, 0217.DVUS02
; CURRENT APPLICATION NUMBER: US/10/658,180
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 09/755,630
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 246
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-658-180-246

```

| Query Match | Similarity | Score | DB | Length | Match | Local Similarity | Pred. No. | 2-be-276 | Mismatches | Indels | Gaps |
|-------------|------------------|---|----------------------------|--------|--------|------------------|-----------|----------|------------|--------|------|
| Best | Local Similarity | 100.0% | 100.0% | 100.0% | 100.0% | 100.0% | 100.0% | 100.0% | 0 | 0 | 0 |
| Match | Similarity | Score | DB | Length | Match | Local Similarity | Pred. No. | 2-be-276 | Mismatches | Indels | Gaps |
| 1128 | Conservative | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Qy | 1 | TCGAGAAAAGAGAGGCTGAGACCTTCATTCGATGATTA | CAAAAAAATGCTGTGCTCTCATTAAG | 60 | | | | | | | |
| Db | 1 | TCGAGAAAAGAGAGGCTGAGACCTTCATTCGATGATTA | CAAAAAAATGCTGTGCTCTCATTAAG | 60 | | | | | | | |
| Qy | 61 | GCACTGCGACATCTTCAGAGTTTGATTAATAACATATAC | GACAAAAGGAGGACGCTACCTGGA | 120 | | | | | | | |
| Db | 61 | GCACTGCGACATCTTCAGAGTTTGATTAATAACATATAC | GACAAAAGGAGGACGCTACCTGGA | 120 | | | | | | | |
| Qy | 121 | CTGCTGTACATTCGATGTTAGTTATATACAGAAAATGAC | CTGATGCGACAACTTCTTATCATGA | 180 | | | | | | | |
| Db | 121 | CTGCTGTACATTCGATGTTAGTTATATACAGAAAATGAC | CTGATGCGACAACTTCTTATCATGA | 180 | | | | | | | |
| Qy | 181 | CTGATTTATATCCTTTCTACAGCTTTTTCAGGCTTGAT | TCCAAAAACAATTAACCTCAGGG | 240 | | | | | | | |
| Db | 181 | CTGATTTATATCCTTTCTACAGCTTTTTCAGGCTTGAT | TCCAAAAACAATTAACCTCAGGG | 240 | | | | | | | |
| Qy | 241 | TTCAAGAAAATGACATTTAAACAGGACAACATCTGAAA | TGATGATGCTTCTGAGGCTTAATA | 300 | | | | | | | |
| Db | 241 | TTCAAGAAAATGACATTTAAACAGGACAACATCTGAAA | TGATGATGCTTCTGAGGCTTAATA | 300 | | | | | | | |
| Qy | 301 | TGGAATTTATGTAACAAGTTGCTGAAAACTTATTTGA | AAGAAACCAAGTTTCCGAAACAATC | 360 | | | | | | | |
| Db | 301 | TGGAATTTATGTAACAAGTTGCTGAAAACTTATTTGA | AAGAAACCAAGTTTCCGAAACAATC | 360 | | | | | | | |
| Qy | 361 | CTGAAACCTATGAGAGAGCTCTTAAGAGGCTTTGCAAA | ATTCCTCTCTGATATGGAAGAAAC | 420 | | | | | | | |
| Db | 361 | CTGAAACCTATGAGAGAGCTCTTAAGAGGCTTTGCAAA | ATTCCTCTCTGATATGGAAGAAAC | 420 | | | | | | | |
| Qy | 421 | TCCAGCAAAACAAGCTTCTTATGGAACAAGGACAGTT | GAGAAATGCTGACTGTTCTTTA | 480 | | | | | | | |
| Db | 421 | TCCAGCAAAACAAGCTTCTTATGGAACAAGGACAGTT | GAGAAATGCTGACTGTTCTTTA | 480 | | | | | | | |
| Qy | 481 | GTATTGATGAGAGTGTGAATTAAGAGGATCATTCGGG | CTACCAATCTTCGAATTTCTTGAG | 540 | | | | | | | |
| Db | 481 | GTATTGATGAGAGTGTGAATTAAGAGGATCATTCGGG | CTACCAATCTTCGAATTTCTTGAG | 540 | | | | | | | |
| Qy | 541 | GACAACTTCAGGAAATGGAACAATATGCAATATGCAAT | ATGCAATTAATTGATGATTA | 600 | | | | | | | |
| Db | 541 | GACAACTTCAGGAAATGGAACAATATGCAATATGCAAT | ATGCAATTAATTGATGATTA | 600 | | | | | | | |
| Qy | 601 | TTGAGAGAAACAATGACAGAGGTTTATGATCTGCGAT | ATGATTAAGTATCTCAATATGAAACA | 660 | | | | | | | |
| Db | 601 | TTGAGAGAAACAATGACAGAGGTTTATGATCTGCGAT | ATGATTAAGTATCTCAATATGAAACA | 660 | | | | | | | |

QY 661 ATGACCCCTTGGCTGCGCAAGAAATTTGACCTTTTACTTGGACATGGCCCTCAGA 720
 DB 661 ATGACCCCTTGGCTGCGCAAGAAATTTGACCTTTTACTTGGACATGGCCCTCAGA 720
 QY 721 TTTTAAATCTAGTGTGCAAAATTTTAGGCCCAAAATATGATGAAAAATATCTTATGCAAG 780
 DB 721 TTTTAAATCTAGTGTGCAAAATTTTAGGCCCAAAATATGATGAAAAATATCTTATGCAAG 780
 QY 781 TTCTTCAAGAAAACTTGGAAACCTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCT 840
 DB 781 TTCTTCAAGAAAACTTGGAAACCTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCT 840
 QY 841 CAAGCTTTCACATCAAAAACAAATTAAGCCAGTAATATTCATAGTCAAAATTTAGCAAACT 900
 DB 841 CAAGCTTTCACATCAAAAACAAATTAAGCCAGTAATATTCATAGTCAAAATTTAGCAAACT 900
 QY 901 CTCAGAAATTTGATGCTAAGATGATGACATTAAGTTATTCACAGCAGCAGCTCCAACT 960
 DB 901 CTCAGAAATTTGATGCTAAGATGATGACATTAAGTTATTCACAGCAGCAGCTCCAACT 960
 QY 961 ATTTTCCTCCGCAATTAATTTGATTAATCTAATATCTAATATGAGATGAATATGAGTTCAATC 1020
 DB 961 ATTTTCCTCCGCAATTAATTTGATTAATCTAATATCTAATATGAGATGAATATGAGTTCAATC 1020
 QY 1021 TTGTTGATGCTGTGCTGCTACTGCTGCTGATCCGGCTTAATATTCATTAAGGCTTGCA 1080
 DB 1021 TTGTTGATGCTGTGCTGCTACTGCTGCTGATCCGGCTTAATATTCATTAAGGCTTGCA 1080
 QY 1081 CGAGACTTGCAAAAAGATCCAGCATTTGCTTCAATTAAGTAAATGAG 1128
 DB 1081 CGAGACTTGCAAAAAGATCCAGCATTTGCTTCAATTAAGTAAATGAG 1128

RESULT 3
 US-10-682-011-20
 ; Sequence 20, Application US/10682011
 ; Publication No. US20040253699A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alibhai, Murtaza
 ; APPLICANT: Rydel, Timothy
 ; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
 ; FILE REFERENCE: 38-21 (51842)B
 ; CURRENT APPLICATION NUMBER: US/10/682,011
 ; PRIOR FILING DATE: 2003-10-09
 ; PRIOR APPLICATION NUMBER: US/09/755,274
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patent version 3.0
 ; SEQ ID NO 20
 ; LENGTH: 1128
 ; TYPE: DNA
 ; ORGANISM: synthetic
 ; FEATURE:
 ; NAME/KEY: DNA
 ; LOCATION: (1)..(1128)
 ; OTHER INFORMATION: pMON3/402 sequence encoding permealtein protein
 ; US-10-682-011-20

Query Match 100.0%; Score 1128; DB 18; Length 1128;
 Best Local Similarity 100.0%; Pred. No. 2,8e-276;
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGAAAAGAGAGCTGAAGCTTCAATGATTAACAAAAAATGCTGTTCTCTCATTAAG 60
 DB 1 TCGAGAAAAGAGAGCTGAAGCTTCAATGATTAACAAAAAATGCTGTTCTCTCATTAAG 60
 QY 61 GCACCTGCACTACTTCAAGATTGATTAACATATACAGAAAAAGAGGCTCACTGGA 120
 DB 61 GCACCTGCACTACTTCAAGATTGATTAACATATACAGAAAAAGAGGCTCACTGGA 120
 QY 121 CTGCTGTACATTGATGATTAGTTATACAGAAATGACTGATGAGCAAGTTCTTACATGA 180
 DB 121 CTGCTGTACATTGATGATTAGTTATACAGAAATGACTGATGAGCAAGTTCTTACATGA 180

DB 121 CTGCTGTACATTGATGATTAGTTATACAGAAATGACTGATGAGCAAGTTCTTACATGA 180
 QY 181 CTGATTAATACCTTTGCTGCTGCTTTTCAAGCTCTGATTTCAAAAACAAATTAACCTCAGG 240
 DB 181 CTGATTAATACCTTTGCTGCTGCTTTTCAAGCTCTGATTTCAAAAACAAATTAACCTCAGG 240
 QY 241 TTCAAGAAAATGCAATTAACAGGCAAACTACTGAAAATGATGATGCTTCTGAGGCTAATA 300
 DB 241 TTCAAGAAAATGCAATTAACAGGCAAACTACTGAAAATGATGATGCTTCTGAGGCTAATA 300
 QY 301 TGAATTTATTAATGATCAAGTTGTGAAAACCTTATTAAGAAACCAAGTTCCGAGACAATC 360
 DB 301 TGAATTTATTAATGATCAAGTTGTGAAAACCTTATTAAGAAACCAAGTTCCGAGACAATC 360
 QY 361 CTGAACCTATGAGAAAGCTCTAAGAGCTTTGCAAAATTTGCTCTGATGAGAAAGAAC 420
 DB 361 CTGAACCTATGAGAAAGCTCTAAGAGCTTTGCAAAATTTGCTCTGATGAGAAAGAAC 420
 QY 421 TCCAGCAAAACAAGCTTTCTTATGACACAGACAGTTGGAGAAATGCTGTTCTTA 480
 DB 421 TCCAGCAAAACAAGCTTTCTTATGACACAGACAGTTGGAGAAATGCTGTTCTTA 480
 QY 481 GATTTGATGAGGTGGAATTAAGAGGATCATTCGCGCTACATTTCTGAATTTCTTGAAG 540
 DB 481 GATTTGATGAGGTGGAATTAAGAGGATCATTCGCGCTACATTTCTGAATTTCTTGAAG 540
 QY 541 GACAACTTGAGAAATGACAAATATGACAGATGCAAGACTTGGAGATTAATTTGATGATTA 600
 DB 541 GACAACTTGAGAAATGACAAATATGACAGATGCAAGACTTGGAGATTAATTTGATGATTA 600
 QY 541 GACAACTTGAGAAATGACAAATATGACAGATGCAAGACTTGGAGATTAATTTGATGATTA 600
 DB 541 GACAACTTGAGAAATGACAAATATGACAGATGCAAGACTTGGAGATTAATTTGATGATTA 600
 QY 601 TTGAGGAAACAAGTACAGAGAGTTTATTTGACTGCTATGATTAAGTATCCAAATGAAAACA 660
 DB 601 TTGAGGAAACAAGTACAGAGAGTTTATTTGACTGCTATGATTAAGTATCCAAATGAAAACA 660
 QY 661 ATGACCCCTTGGCTGCTGCGCAAGAAATTTGACCTTTTACTTGGACATGGCCCTCAGA 720
 DB 661 ATGACCCCTTGGCTGCTGCGCAAGAAATTTGACCTTTTACTTGGACATGGCCCTCAGA 720
 QY 721 TTTTAAATCTAGTGTGCAAAATTTTAGGCCCAAAATATGATGAAAAATATCTTATGCAAG 780
 DB 721 TTTTAAATCTAGTGTGCAAAATTTTAGGCCCAAAATATGATGAAAAATATCTTATGCAAG 780
 QY 781 TTCTTCAAGAAAACTTGGAAACCTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCT 840
 DB 781 TTCTTCAAGAAAACTTGGAAACCTGTGTGATCAAGCTTTGACAGAAAGTTGTCTATCT 840
 QY 841 CAAGCTTTCACATCAAAAACAAATTAAGCCAGTAATATTCATAGTCAAAATTTAGCAAACT 900
 DB 841 CAAGCTTTCACATCAAAAACAAATTAAGCCAGTAATATTCATAGTCAAAATTTAGCAAACT 900
 QY 901 CTCAGAAATTTGATGCTAAGATGATGACATTAAGTTATTCACAGCAGCAGCTCCAACT 960
 DB 901 CTCAGAAATTTGATGCTAAGATGATGACATTAAGTTATTCACAGCAGCAGCTCCAACT 960
 QY 961 ATTTTCCTCCGCAATTAATTTGATTAATCTAATATCTAATATGAGATGAATATGAGTTCAATC 1020
 DB 961 ATTTTCCTCCGCAATTAATTTGATTAATCTAATATCTAATATGAGATGAATATGAGTTCAATC 1020
 QY 1021 TTGTTGATGCTGTGCTGCTACTGCTGCTGATCCGGCTTAATATTCATTAAGGCTTGCA 1080
 DB 1021 TTGTTGATGCTGTGCTGCTACTGCTGCTGATCCGGCTTAATATTCATTAAGGCTTGCA 1080
 QY 1081 CGAGACTTGCAAAAAGATCCAGCATTTGCTTCAATTAAGTAAATGAG 1128
 DB 1081 CGAGACTTGCAAAAAGATCCAGCATTTGCTTCAATTAAGTAAATGAG 1128

RESULT 4
 US-09-755-630A-258
 ; Sequence 258, Application US/09755630A
 ; Publication No. US20030194399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALIBHAI, MURTAZA F.

APPLICANT: ASTWOOD, JAMES D.
APPLICANT: SAMPSON, HUGH A.
APPLICANT: MCMHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTTEINS
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
CURRENT APPLICATION NUMBER: US/09/755,630A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 293
SOFTWARE: PatentIn version 3.0
SEQ ID NO 258
LENGTH: 1128
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-755-630A-258

Query Match 91.9%; Score 1036.2; DB 10; Length 1128;
Best Local Similarity 99.2%; Pred. No. 6,4e-253;
Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

77 AGAGTTGATTAATAACATATACAGCAAAAGAGGAGCTGACCTGACCTGATGATGAT 136
11 AGAGGCTGAGCTACATATACAGCAAAAGAGGAGCTGACCTGATGATGATGAT 70
137 GTTATGTTATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 196
71 GTTATGTTATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 130
197 TACTGCTTTTCAAGCTCTGATTCATTAATACTCAAGGCTTCAAGAAATGATGAT 256
131 TACTGCTTTTCAAGCTCTGATTCATTAATACTCAAGGCTTCAAGAAATGATGAT 190
257 AACAGGCAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316
191 AACAGGCAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
317 AGTTGGTGAATACTTATGTAAGAAACAGTTTCCGAAGCAATCTGAAACCTATGAGA 376
251 AGTTGGTGAATACTTATGTAAGAAACAGTTTCCGAAGCAATCTGAAACCTATGAGA 310
377 AGCTCTAAGAGGTTTGGCAAAATGCTCTCTGATAGGAAGAACTCCGAGCAAAAGC 436
311 AGCTCTAAGAGGTTTGGCAAAATGCTCTCTGATAGGAAGAACTCCGAGCAAAAGC 370
437 TTCTTATGACCAAGGACATGTTGGAGAAATGATGATGATGATGATGATGATGATGAT 436
371 TTCTTATGACCAAGGACATGTTGGAGAAATGATGATGATGATGATGATGATGATGAT 430
497 AATTAGAGGATATTCCTGCTACCAATTCCTGCAATTTCTTGAAGCAATCTGAGAAAT 556
431 AATTAGAGGATATTCCTGCTACCAATTCCTGCAATTTCTTGAAGCAATCTGAGAAAT 490
557 GGAACAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
491 GGAACAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
617 AGAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 676
551 AGAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
677 TGGCAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736
611 TGGCAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
737 TCAAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 796
671 TCAAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730
797 TGAAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 856

731 TGAAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790
857 AACAAATTAAGCAGATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 916
791 AACAAATTAAGCAGATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850
917 TAAGAT 976
851 TAAGAT 910
977 CTGTTGTTATTAATATGAT 1036
911 CTGTTGTTATTAATATGAT 970
1037 TGGTACTGTTGCTGAT 1096
971 TGGTACTGTTGCTGAT 1030
1097 GGATCCAGATTTGCTTCAATTAAGTAAAT 1125
1031 GGATCCAGATTTGCTTCAATTAAGTAAAT 1059

RESULT 5
US-10-658-180-258
Sequence 258, Application US/10658180
Publication No. US20040216187A1
GENERAL INFORMATION:
APPLICANT: ALIBHAI, MURTAZA F.
APPLICANT: ASTWOOD, JAMES D.
APPLICANT: SAMPSON, HUGH A.
APPLICANT: MCMHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTTEINS
FILE REFERENCE: 11899.0217.DVUS02
CURRENT APPLICATION NUMBER: US/10/658,180
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: US 09/755,630
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 295
SOFTWARE: PatentIn version 3.2
SEQ ID NO 258
LENGTH: 1128
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-658-180-258
Query Match 91.9%; Score 1036.2; DB 18; Length 1128;
Best Local Similarity 99.2%; Pred. No. 6,4e-253;
Matches 1041; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
77 AGAGTTGATTAATAACATATACAGCAAAAGAGGAGCTGACCTGACCTGATGATGAT 136
11 AGAGGCTGAGCTACATATACAGCAAAAGAGGAGCTGACCTGATGATGATGATGAT 70
137 GTTATGTTATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
71 GTTATGTTATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 130
197 TACTGCTTTTCAAGCTCTGATTCATTAATACTCAAGGCTTCAAGAAATGATGAT 256
131 TACTGCTTTTCAAGCTCTGATTCATTAATACTCAAGGCTTCAAGAAATGATGAT 190
257 AACAGGCAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316
191 AACAGGCAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
317 AGTTGGTGAATACTTATGTAAGAAACAGTTTCCGAAGCAATCTGAAACCTATGAGA 376
251 AGTTGGTGAATACTTATGTAAGAAACAGTTTCCGAAGCAATCTGAAACCTATGAGA 310

| | | | |
|----|------|---|------|
| QY | 377 | AGCCTTAAAGAGGTTTGCAAAATGCTCTCGATGTGAAAGAACTCCGAGAAACAAAGC | 436 |
| Db | 311 | AGCTTTAAAGAGGTTTGCAAAATGCTCTCGATGTGAAAGAACTCCGATCAACAAAGC | 370 |
| QY | 437 | TTCTTATGACACAGACAGTGGGAGAAATGATGATCTGTTCTAGTATTTGATGAGGTGC | 496 |
| Db | 371 | TTCTTATGACACAGACAGTGGGAGAAATGATGATCTGTTCTAGTATTTGATGAGGTGC | 430 |
| QY | 497 | AATTAGAGGATCATTCGCGCTACCATTTCTGGAATTTCTTGAGGACAATTCAAGAAAT | 556 |
| Db | 431 | AATTAGAGGATCATTCGCGCTACCATTTCTGGAATTTCTTGAGGACAATTCAAGAAAT | 490 |
| QY | 557 | GGAACAATPATGCAATGCAAGACTTGACGATTACTTTGATGAATTTGAGGAAACAAGAC | 616 |
| Db | 491 | GGAACAATPATGCAATGCAAGACTTGACGATTACTTTGATGAATTTGAGGAAACAAGAC | 550 |
| QY | 617 | AGAGAGTTTATGACCTGCTATGATAGTACTCCAAATGAAAAACATCGACCTTGTCTGC | 676 |
| Db | 551 | AGAGAGTTTATGACCTGCTATGATAGTACTCCAAATGAAAAACATCGACCTTGTCTGC | 610 |
| QY | 677 | TGCCAAGAATTTGTAACCTTTTACTTGGAACATGCGCCCTGAGATTTTAAATCTGATGC | 736 |
| Db | 611 | TGCCAAGAATTTGTAACCTTTTACTTGGAACATGCGCCCTGAGATTTTAAATCTGATGC | 670 |
| QY | 737 | TGCAATTTTGGGCCCAAAATATGATGAAAAATCTTATGCAAGTCTTCAAGAAAAACT | 796 |
| Db | 671 | TGCAATTTTGGGCCCAAAATATGATGAAAAATCTTATGCAAGTCTTCAAGAAAAACT | 730 |
| QY | 797 | TGAGAAACTCGTNGCATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCA | 856 |
| Db | 731 | TGAGAAACTCGTNGCATCAAGCTTTGACAGAAAGTTGTCATCTCAAGCTTTGACATCA | 790 |
| QY | 857 | AACAAATPAGCAGTAAATATTCCTAAGTCAATTAGCAAACTCTCCAGAAATGATGC | 916 |
| Db | 791 | AACAAATPAGCAGTAAATATTCCTAAGTCAAACTCTCCAGAAATGATGC | 850 |
| QY | 917 | TAAATGATATCAGTAAGTTATATTCACAGCAGCAGCTCAACATATTTTCCCGCATTA | 976 |
| Db | 851 | TAAATGATATCAGTAAGTTATATTCACAGCAGCAGCTCAACATATTTTCCCGCATTA | 910 |
| QY | 977 | CTTGTGTTACTATATCTAGTAAATGAGATGATATGATTCATCTTGTGTGATGCTGCT | 1038 |
| Db | 911 | CTTGTGTTACTATATCTAGTAAATGAGATGATATGATTCATCTTGTGTGATGCTGCT | 970 |
| QY | 1037 | TGCTACTGTTGCTGATCCGCGCTTATATTCATTAGCGTTGCAACGAGACTTGCACAAA | 1096 |
| Db | 971 | TGCTACTGTTGCTGATCCGCGCTTATATTCATTAGCGTTGCAACGAGACTTGCACAAA | 1030 |
| QY | 1097 | GGATCCAGCATTTGCTTCAATTTAGGTAT | 1125 |
| Db | 1031 | GGATCCAGCATTTGCTTCAATTTAGGTAT | 1059 |

RESULT 6
 US-10-682-011-26
 , Sequence 26, Application US/10682011
 , Publication No. US20040253699A1
 , GENERAL INFORMATION:
 , APPLICANT: Alibhai, Murtaza
 , APPLICANT: Rydel, Timothy
 , TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
 , FILE REFERENCE: 38-21 (51842)B
 , CURRENT APPLICATION NUMBER: US/10/682,011
 , CURRENT FILING DATE: 2003-10-03
 , PRIOR APPLICATION NUMBER: US/09/755,274
 , PRIOR FILING DATE: 2001-01-05
 , NUMBER OF SEQ ID NOS: 60
 , SOFTWARE: PatentIn version 3.0
 , SEQ ID NO 26
 , LENGTH: 1128
 , TYPE: DNA
 , ORGANISM: synthetic

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; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1) ..(1128)
; OTHER INFORMATION: pMON57407 sequence encoding permutein protein
US-10-682-011-26

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| | | | | |
|-----------------------|--------------|--------------------|---------------|--------------|
| Query Match | 91.9% | Score 1036.2; | DB 18; | Length 1128; |
| Best Local Similarity | 99.2%; | Pred. No. 64e-253; | | |
| Matches 1041; | Conservative | 0; | Mismatches 8; | Indels 0; |
| | | | Gaps | 0; |

| | | | |
|----|-----|--|------|
| QY | 77 | AGAGTTTGATATAAAACATATATACGCAAAAAGAGCAGCTACTTGAGCTGCTGATCATTTGGAT | 136 |
| Db | 11 | AGAGGCTGAACTCATATATACGCAAAAAGAGCAGCTACTTGAGCTGCTGATCATTTGGAT | 70 |
| QY | 137 | GTTAGTTATACAGAAAAATGACTGATGCGAGCAAGTCTTACATGATCTGATTTATTAACCTTTC | 196 |
| Db | 71 | GTTAGTTATACAGAAAAATGACTGATGCGAGCAAGTCTTACATGATCTGATTTATTAACCTTTC | 130 |
| QY | 197 | TACTGCTTTTCAAGCTCTTGATTCGAAAAACAATTACCTCAGGGTTCAAGAAAAATGCAATT | 256 |
| Db | 131 | TACTGCTTTTCAAGCTCTTGATTCGAAAAACAATTACCTCAGGGTTCAAGAAAAATGCAATT | 190 |
| QY | 257 | AACAGGCAACACTACTGAAATGAGATGATGCTTTCGAGCTAAATATGAAATTAATTAGTACA | 316 |
| Db | 191 | AACAGGCAACACTACTGAAATGAGATGATGCTTTCGAGCTAAATATGAAATTAATTAGTACA | 250 |
| QY | 317 | AGTTGCTAATAAAGCTTATGGAAGAAACAGGTTTCGAAACAAATCCGAAACCTATGAGAGA | 376 |
| Db | 251 | AGTTGCTAATAAAGCTTATGGAAGAAACAGGTTTCGAAACAAATCCGAAACCTATGAGAGA | 310 |
| QY | 377 | AGCTCTAAGAAGGTTTGGCAAAATTTGCTCTCGATGAGAAGAACTCCAGCAAAACAAAGC | 436 |
| Db | 311 | AGCTCTAAGAAGGTTTGGCAAAATTTGCTCTCGATGAGAAGAAACCTCGATCAAAACAAAGC | 370 |
| QY | 437 | TTCTTATGGAACGAGACAGCTTGGAGAAATGCTGACTTTCTTAGTATTTGATGAGAGTGG | 496 |
| Db | 371 | TTCTTATGGAACGAGACAGCTTGGAGAAATGCTGACTTTCTTAGTATTTGATGAGAGTGG | 430 |
| QY | 497 | AATTAGAGGAGCAATTCGGGCTACCATTTCTGGAATTTCTGGAAGAGCAACTCAGAGAAAT | 556 |
| Db | 431 | AATTAGAGGAGCAATTCGGGCTACCATTTCTGGAATTTCTGGAAGAGCAACTCAGAGAAAT | 490 |
| QY | 557 | GGACATATATCAGATGCAAGCTTGCAGATTACTTTGATGAAATTTGAGAGAAACAAGTAC | 616 |
| Db | 491 | GGACATATATCAGATGCAAGCTTGCAGATTACTTTGATGAAATTTGAGAGAAACAAGTAC | 550 |
| QY | 617 | AGGAGGTTTATTTGACTGCTATGATAGTATCTCCAAATGAAAAACAATCGACTTTGCTGCG | 676 |
| Db | 551 | AGGAGGTTTATTTGACTGCTATGATAGTATCTCCAAATGAAAAACAATCGACTTTGCTGCG | 610 |
| QY | 677 | TGCCAAGAAATTTGATACCTTTTACTTGGAACATGGCCCTCAGATTTTAAATCCTAGTGG | 736 |
| Db | 611 | TGCCAAGAAATTTGATACCTTTTACTTGGAACATGGCCCTCAGATTTTAAATCCTAGTGG | 670 |
| QY | 737 | TCAAATTTTAAAGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAAACT | 796 |
| Db | 671 | TCAAATTTTAAAGCCCAAAATATGATGAAAAATATCTTATGCAAGTTCTTCAAGAAAAACT | 730 |
| QY | 797 | TGAGAAACCTCGTGTGCATCAAGCTTTTGACAGAAAGTTGTCAATCTCAAGCTTTGACATCA | 856 |
| Db | 731 | TGAGAAACCTCGTGTGCATCAAGCTTTTGACAGAAAGTTGTCAATCTCAAGCTTTGACATCA | 790 |
| QY | 857 | AACAAATTAAGCAGTAATATTCAGTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGCG | 916 |
| Db | 791 | AACAAATTAAGCAGTAATATTCAGTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGCG | 850 |
| QY | 917 | TAAAGTGTATGACATTAAGTTATTCACAGCAGCAGCTCCAAACATATTTTCTCCGCATTA | 976 |
| Db | 851 | TAAAGTGTATGACATTAAGTTATTCACAGCAGCAGCTCCAAACATATTTTCTCCGCATTA | 910 |
| QY | 977 | CTTTGTTACTAATCTACTAGTAAATGAGATGAAATATGAGTTCAATCTGTGATGGGCTGT | 1033 |
| Db | 911 | CTTTGTTACTAATCTACTAGTAAATGAGATGAAATATGAGTTCAATCTGTGATGGGCTGT | 970 |

QY 1037 TGTACTGTTGCTGATCCGGCGTTATTCATTACGTTGCAACAGACTTGCAACAAA 1096
DB 971 TGTACTGTTGCTGATCCGGCGTTATTCATTACGTTGCAACAGACTTGCAACAAA 1030
QY 1097 GGATCCAGCATTTGCTTCAATTAGGTAAT 1125
DB 1031 GGATCCAGCATTTGCTTCAATTAGGTAAT 1059

RESULT 7

US-09-755-630A-250
; Sequence 250, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCHESTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT21.7)
; CURRENT APPLICATION NUMBER: US/09/755,630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-755-630A-250

Query Match 85.4%; Score 963.4; DB 10; Length 1128;
Best Local Similarity 99.9%; Pred. No. 2.1e-234;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTACAGAGTTT 83
DB 159 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTACAGAGTTT 218
QY 84 GATTAACATATACAGCAAAAGAGGAGCTTACCTGATGCTGTATACATTTAGTATTAGTT 143
DB 219 GATTAACATATACAGCAAAAGAGGAGCTTACCTGATGCTGTATACATTTAGTATTAGTT 278
QY 144 ATTCAGAAATATGCTATGAGCAAGTTCTTACATGATGATTAATTAATTAATTAATTAATTA 203
DB 279 ATTCAGAAATATGCTATGAGCAAGTTCTTACATGATGATTAATTAATTAATTAATTAATTA 338
QY 204 TTTCAAGCTCTTATTTCAAAAAACAATTAATCTCAGGGTTCAAAAAATGATTAACAGGC 263
DB 339 TTTCAAGCTCTTATTTCAAAAAACAATTAATCTCAGGGTTCAAAAAATGATTAACAGGC 398
QY 264 ACAACTACTGAAATGATGATGCTTCTGAGGCTTAATATGAAATTAATTAATTAATTAATTA 323
DB 399 ACAACTACTGAAATGATGATGCTTCTGAGGCTTAATATGAAATTAATTAATTAATTAATTA 458
QY 324 GAAACTTATTTGAAAGAAACAGTTTCCGAGAACATCTGAAACCTATATGAGAGGCTCTA 383
DB 459 GAAACTTATTTGAAAGAAACAGTTTCCGAGAACATCTGAAACCTATATGAGAGGCTCTA 518
QY 384 AAGAGGTTTGCAAAATGCTCTGATAGAGAAACTCCGAGCAAAACAAGCTTCTAT 443
DB 519 AAGAGGTTTGCAAAATGCTCTGATAGAGAAACTCCGAGCAAAACAAGCTTCTAT 578
QY 444 GAGCAGAGCAGTTGGAGAAATGATGATGCTTCTTATATGATGATGAGGTGGAATTTAGA 503
DB 579 GAGCAGAGCAGTTGGAGAAATGATGATGCTTCTTATATGATGATGAGGTGGAATTTAGA 638
QY 504 GGATCATTTCCGGCTACATTTCTGCAATTTCTTGAAGAGCAATTTGAGAAATGAGCAAT 563
DB 219 GATTAACATATACAGCAAAAGAGGAGCTTACCTGAGCTGCTATGATGATGATGATGATGAT 278

DB 639 GGATCATTTCCGGCTACATTTCTGCAATTTCTTGAAGAGCAATTTGAGAAATGAGCAAT 698
QY 564 AATGAGATGCAAGACTTGCAGATTTACTTGTATGATGATGAGAGAAACAATGACAGAGGT 623
DB 699 AATGAGATGCAAGACTTGCAGATTTACTTGTATGATGATGAGAGAAACAATGACAGAGGT 758
QY 624 TTAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683
DB 759 TTAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
QY 684 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 743
DB 819 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
QY 744 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAAACTTGAGAA 803
DB 879 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAAACTTGAGAA 938
QY 804 ACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
DB 939 ACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 998
QY 864 AAGCAGATATATTTCACTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGATGATGATG 923
DB 999 AAGCAGATATATTTCACTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGATGATGATG 1058
QY 924 TATGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 983
DB 1059 TATGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
QY 984 ACTTA 988
DB 1119 ACTTA 1123

RESULT 8

US-10-658-180-250
; Sequence 250, Application US/10658180
; Publication No. US20040216187A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCHESTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.DVUS02
; CURRENT APPLICATION NUMBER: US/10/658,180
; PRIOR FILING DATE: 2003-09-09
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 250
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-658-180-250

Query Match 85.4%; Score 963.4; DB 10; Length 1128;
Best Local Similarity 99.9%; Pred. No. 2.1e-234;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTACAGAGTTT 83
DB 159 TCATTGAATTTACAAAAAATGCTGTTGCTCTCATTTAGGCACTGGCACTTACAGAGTTT 218
QY 84 GATTAACATATACAGCAAAAGAGGAGCTTACCTGAGCTGCTATGATGATGATGATGATGATGAT 143
DB 219 GATTAACATATACAGCAAAAGAGGAGCTTACCTGAGCTGCTATGATGATGATGATGATGATGAT 278

144 ATACAGAAAAAGTGTGACGAAAGTCTTACATGACTGATTTATTCCTTTCTACTGCT 203
279 ATACAGAAAAAGTGTGACGAAAGTCTTACATGACTGATTTATTCCTTTCTACTGCT 338
204 TTTCAGCTCTGATTTCAAAAAACAATTACTCGGGTTCAAGAAATGATTAACAGGC 263
339 TTTCAGCTCTGATTTCAAAAAACAATTACTCGGGTTCAAGAAATGATTAACAGGC 398
264 ACAACTCTGAATGATGATGCTTCTGAGGCTAATATGAAATTAATAGTCAAGTGGT 323
399 ACAACTCTGAATGATGATGCTTCTGAGGCTAATATGAAATTAATAGTCAAGTGGT 458
324 GAAACCTTATTTGAAGAAACAGTTTCCGAGACAACTCTGAAACCTTATGAGAGCTCTA 383
459 GAAACCTTATTTGAAGAAACAGTTTCCGAGACAACTCTGAAACCTTATGAGAGCTCTA 518
384 AAGAGTTTGCATAAATGCTCTCTGATAGAGAAACCTCGAGCAAAACAAGCTTCTTAT 443
519 AAGAGTTTGCATAAATGCTCTCTGATAGAGAAACCTCGAGCAAAACAAGCTTCTTAT 578
444 GACACGAGAGAGTTGGAGAAATGCTGATCTGATATGATATGATGAGTGGAAATTTGA 503
579 GACACGAGAGAGTTGGAGAAATGCTGATCTGATATGATATGATGAGTGGAAATTTGA 638
504 GGGATCTTCCGCTACCATTTCTGAAATTTCTTGAAGGACAACTTCAGAGAAATGAGCAAT 563
639 GGGATCTTCCGCTACCATTTCTGAAATTTCTTGAAGGACAACTTCAGAGAAATGAGCAAT 698
564 AATGACAGTCAAGACTTGACGATTTACTTGTATTTGAGAGAAACAAGTACAGAGGT 623
699 AATGACAGTCAAGACTTGACGATTTACTTGTATTTGAGAGAAACAAGTACAGAGGT 758
624 TTATTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683
759 TTATTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
684 GAAATTTGATCTTCTTCTGAAACATGAGCCCTCAGATTTTAAATCCGATGATCAATTT 743
819 GAAATTTGATCTTCTTCTGAAACATGAGCCCTCAGATTTTAAATCCGATGATCAATTT 878
744 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAAGA 803
879 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAAGA 938
804 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
939 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 998
864 AAGCAGTATATTTCACTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGATGATG 923
999 AAGCAGTATATTTCACTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGATGATG 1058
924 TATGACATTAAGTATTTCAAGAGAGAGCTCAACATATTTTCTCCGCAATTAATTTGTT 983
1059 TATGACATTAAGTATTTCAAGAGAGAGCTCAACATATTTTCTCCGCAATTAATTTGTT 1118
984 ACTAA 988
1119 ACTTA 1123

RESULT 9

US-10-682-011-22
; Sequence 22, Application US/10682011
; Publication No. US20040253699A1
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murfaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/10/682,011
; CURRENT FILING DATE: 2003-10-09

PRIOR APPLICATION NUMBER: US/09/755,274
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1)..(1128)
; OTHER INFORMATION: pMON37405 sequence encoding permuterin protein
US-10-682-011-22

Query Match 85.4%; Score 963.4; DB 18; Length 1128;
Best Local Similarity 99.9%; Pred. NO. 2.1e-224;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

24 TCATTGAATTTACAAAAAATGCTGCTGCTCAATTAGGCACTGGCACTACTTCAAGTGT 83
159 TCATTGAATTTACAAAAAATGCTGCTGCTCAATTAGGCACTGGCACTACTTCAAGTGT 218
84 GATTAACATATACGCAAAAGAGGAGCTACTGAGCTGCTGATCAATTGGATTTAGTT 143
219 GATTAACATATACGCAAAAGAGGAGCTACTGAGCTGCTGATCAATTGGATTTAGTT 278
144 ATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 203
279 ATACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 338
204 TTTCAGCTCTGATTTCAAAAAACAATTACTCGGGTTCAAGAAATGATTAACAGGC 263
339 TTTCAGCTCTGATTTCAAAAAACAATTACTCGGGTTCAAGAAATGATTAACAGGC 398
264 ACAACTCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323
399 ACAACTCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 458
324 GAAACCTTATTTGAAGAAACAGTTTCCGAGACAACTCTGAAACCTTATGAGAGCTCTA 383
459 GAAACCTTATTTGAAGAAACAGTTTCCGAGACAACTCTGAAACCTTATGAGAGCTCTA 518
384 AAGAGTTTGCATAAATGCTCTCTGATAGAGAAACCTCGAGCAAAACAAGCTTCTTAT 443
519 AAGAGTTTGCATAAATGCTCTCTGATAGAGAAACCTCGAGCAAAACAAGCTTCTTAT 578
444 GACACGAGAGAGTTGGAGAAATGCTGATCTGATATGATATGATGATGATGATGATGATGAT 503
579 GACACGAGAGAGTTGGAGAAATGCTGATCTGATATGATATGATGATGATGATGATGATGAT 638
504 GGGATCTTCCGCTACCATTTCTGAAATTTCTTGAAGGACAACTTCAGAGAAATGAGCAAT 563
639 GGGATCTTCCGCTACCATTTCTGAAATTTCTTGAAGGACAACTTCAGAGAAATGAGCAAT 698
564 AATGACAGTCAAGACTTGACGATTTACTTGTATTTGAGAGAAACAAGTACAGAGGT 623
699 AATGACAGTCAAGACTTGACGATTTACTTGTATTTGAGAGAAACAAGTACAGAGGT 758
624 TTATTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683
759 TTATTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
684 GAAATTTGATCTTCTTCTGAAACATGAGCCCTCAGATTTTAAATCCGATGATCAATTT 743
819 GAAATTTGATCTTCTTCTGAAACATGAGCCCTCAGATTTTAAATCCGATGATCAATTT 878
744 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAAGA 803
879 TTAGGCCCAAAATATGATGAGAAATATCTTATGCAAGTTCTTCAAGAAAACTTGAAGA 938
804 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
939 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 998

| | | | |
|---|------|---|------|
| OY | 144 | TTACGAAAAAGACGTGACGAAAGTCTTACAGCTGATATTACCTTCTAGCT | 203 |
| Db | 333 | ATACGAAAAAGACGTGACGAAAGTCTTACAGCTGATATTACCTTCTAGCT | 392 |
| OY | 204 | TTTCAAGCTTGGATTCCAAAAACAATTACCTGAGGTTCAAGAAAATGCAATTAACGAGC | 263 |
| Db | 393 | TTTCAAGCTTGGATTCCAAAAACAATTACCTGAGGTTCAAGAAAATGCAATTAACGAGC | 452 |
| OY | 264 | ACAACCTAGTGAATGATGCTTCTGAGGCTAATATGGAATTATTTGTAACAAGTGGT | 323 |
| Db | 453 | ACAACCTAGTGAATGATGCTTCTGAGGCTAATATGGAATTATTTGTAACAAGTGGT | 512 |
| OY | 324 | GAAACTTATGGAAGAAACAGTTTCCGAAGACATCTCGAAACCTATGAGGAAGCTCTA | 383 |
| Db | 513 | GAAACTTATGGAAGAAACAGTTTCCGAAGACATCTCGAAACCTATGAGGAAGCTCTA | 572 |
| OY | 384 | AAGAGTTTGCAAAATTGCTCTCTGATAGGAAGAAAGTCCGAGCAACAAAGCTCTTAT | 443 |
| Db | 573 | AAGAGTTTGCAAAATTGCTCTCTGATAGGAAGAAAGTCCGAGCAACAAAGCTCTTAT | 632 |
| OY | 444 | GGAACAGGACAGTTGGGAGAAATGGTGAATGTTCTTAGATTTGAGAGGTGGAAATTGGA | 503 |
| Db | 633 | GGAACAGGACAGTTGGGAGAAATGGTGAATGTTCTTAGATTTGAGAGGTGGAAATTGGA | 692 |
| OY | 504 | GGGATCATTTCCGGCTACCATTTCTGAAATTTCTTTGGAAGACAACCTTCAGAAATGACAAAT | 563 |
| Db | 693 | GGGATCATTTCCGGCTACCATTTCTGAAATTTCTTTGGAAGACAACCTTCAGAAATGACAAAT | 752 |
| OY | 564 | AATGACAGTGCAGACCTTGCAGATTACTTTGATGTAATTTGAGAGAACAGTACAGAGGT | 623 |
| Db | 753 | AATGACAGTGCAGACCTTGCAGATTACTTTGATGTAATTTGAGAGAACAGTACAGAGGT | 812 |
| OY | 624 | TTATTTGATGCTATAGATATAGTATCTCCAAATGAAAACATTCACCTTTGCTGCTGCCAA | 683 |
| Db | 813 | TTATTTGATGCTATAGATATAGTATCTCCAAATGAAAACATTCACCTTTGCTGCTGCCAA | 872 |
| OY | 684 | GAATTTGACCTTTTAACTTTCGAAATGAGCCCTCAGATTTTAAATCTAGTGGTCAAAAT | 743 |
| Db | 873 | GAATTTGACCTTTTAACTTTCGAAATGAGCCCTCAGATTTTAAATCTAGTGGTCAAAAT | 932 |
| OY | 744 | TTAGGCCCAAAATATGATGAAAATATCTTATGCAAGTTCTTCAGAAAAAAGTTGGAGA | 803 |
| Db | 933 | TTAGGCCCAAAATATGATGAAAATATCTTATGCAAGTTCTTCAGAAAAAAGTTGGAGA | 992 |
| OY | 804 | ACTGCTGTCATCAAGCTTTGACAGAGTGTCACTCAAGCTTTGACATCAAAACAAT | 863 |
| Db | 993 | ACTGCTGTCATCAAGCTTTGACAGAGTGTCACTCAAGCTTTGACATCAAAACAAT | 1055 |
| OY | 864 | AAGCAGATATATTCATCAATGCAATTTAGCAAACTCCAGAAATGATGATGCTAAGATG | 923 |
| Db | 1053 | AAGCAGATATATTCATCAATGCAATTTAGCAAACTCCAGAAATGATGATGCTAAGATG | 1112 |
| OY | 924 | TATGACATA 932 | |
| Db | 1113 | TATGACATA 1121 | |
| RESULT 12 | | | |
| US-10-682-011-24 | | | |
| ; Sequence 24, Application US/10682011 | | | |
| ; Publication No. US20040253699A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Alibhai, Murtaza | | | |
| ; APPLICANT: Rydel, Timothy | | | |
| ; TITLE OF INVENTION: Insect Inhibitory Lipid Aoyl Hydrolases | | | |
| ; FILE REFERENCE: 38-21 (51842)B | | | |
| ; CURRENT APPLICATION NUMBER: US/10/682,011 | | | |
| ; CURRENT FILING DATE: 2003-10-09 | | | |
| ; PRIOR APPLICATION NUMBER: US/09/755,274 | | | |
| ; PRIOR FILING DATE: 2001-01-05 | | | |
| ; NUMBER OF SEQ ID NOS: 60 | | | |
| ; SOFTWARE: PatentIn version 3.0 | | | |

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; SEQ ID NO 24
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: DNA
; LOCATION: (1)..(1128)
; OTHER INFORMATION: pMON37406 sequence encoding permutein protein
US-10-682-011-24

Query Match      80.6%; Score 909; DB 18; Length 1128;
Best Local Similarity 100.0%; Pred. No. 1.5e-220;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24 TCATTGAATTCGAAAAAATGCTGTGTGCTCATTTAGGCACATGGCAGCTTTCAGAGCTT 83
DB      213 TCATTGAATTCGAAAAAATGCTGTGTGCTCATTTAGGCACATGGCAGCTTTCAGAGCTT 272

QY      84 GATAAAAATATATACGCAAAAGAGGACAGCTACCTGAGCTGCTGATATTTGATGTTAGTT 143
DB      273 GATAAAAATATATACGCAAAAGAGGACAGCTACCTGAGCTGCTGATATTTGATGTTAGTT 332

QY      144 ATACAGAAAAATGAGCTGATGACGAAAGTTCTTACATGACTGATTTATACCTTTCTACTGCT 203
DB      333 ATACAGAAAAATGAGCTGATGACGAAAGTTCTTACATGACTGATTTATACCTTTCTACTGCT 392

QY      204 TTTCAAGCTCTTGATTCAAAAAACAATTACTCCAGGGTTTCAAGAAAATGCATTACAGGC 263
DB      393 TTTCAAGCTCTTGATTCAAAAAACAATTACTCCAGGGTTTCAAGAAAATGCATTACAGGC 452

QY      284 ACAACTACTGAAATGAGATGATGCTTCGAGGCTAATATGAAATTAATTAAGTACAGTGGT 323
DB      453 ACAACTACTGAAATGAGATGATGCTTCGAGGCTAATATGAAATTAATTAAGTACAGTGGT 512

QY      324 GAAAACTATTGGAAGAAACAGATTTCGCAACAATCCCTGAACCTATGAGAAAGCTCTA 383
DB      513 GAAAACTATTGGAAGAAACAGATTTCGCAACAATCCCTGAACCTATGAGAAAGCTCTA 572

QY      384 AAGAGTTTGGAAAAATTGCTCTCTGTATGGAAGAACTCCGAGCAACAAGCTTCTTAT 443
DB      573 AAGAGTTTGGAAAAATTGCTCTCTGTATGGAAGAACTCCGAGCAACAAGCTTCTTAT 632

QY      444 GGAACGAGACAGTTGGGGAATATGTGATCTGTATTTGATTTGAGAGTGAATTAAGA 503
DB      633 GGAACGAGACAGTTGGGGAATATGTGATCTGTATTTGAGAGTGAATTAAGA 692

QY      504 GGGATCATTCGGGCTACCACTCTCGAATTTCTTGAAGACAATTCAGGAATGACAAAT 563
DB      693 GGGATCATTCGGGCTACCACTCTCGAATTTCTTGAAGACAATTCAGGAATGACAAAT 752

QY      564 AATGCAGATGCAAGACTTCGAGATTACTCTTGATGTAATTGAGAGAACAAATGACAGAGT 623
DB      753 AATGCAGATGCAAGACTTCGAGATTACTCTTGATGTAATTGAGAGAACAAATGACAGAGT 812

QY      624 TTATTGACTGCTATGATTAAGTACTCCAAATGAAAACAATGCACCTTTGCTGCTGCCAA 683
DB      813 TTATTGACTGCTATGATTAAGTACTCCAAATGAAAACAATGCACCTTTGCTGCTGCCAA 872

QY      684 GAAATTTGACCTTTTAACTTGGAACATGGCCCTGAGATTTTAAATCCTAGTGGTCAAAAT 743
DB      873 GAAATTTGACCTTTTAACTTGGAACATGGCCCTGAGATTTTAAATCCTAGTGGTCAAAAT 932

QY      744 TTAGGCCCAAAATATGATGAAAAATATCTTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 803
DB      933 TTAGGCCCAAAATATGATGAAAAATATCTTTATGCAAGTTCTTCAAGAAAACTTGGAGAA 992

QY      804 ACTGCTGTGCATCAAGCTTTGACGAAGTGTCACTTCAGCTTTGACATGAAAACAAAAT 863
DB      993 ACTGCTGTGCATCAAGCTTTGACGAAGTGTCACTTCAGCTTTGACATGAAAACAAAAT 1052

QY      864 AAGCAGAAATATTTCACTTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGCTTAAGTG 923
DB      1053 AAGCAGAAATATTTCACTTAAGTCAAAATTTAGCAAACTCTCAGAAATTTGATGCTTAAGTG 1112

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using bw model

Run on: April 8, 2005, 07:18:52 ; Search time 175 Seconds
(without alignments)
808.882 Million cell updates/sec

Title: US-10-658-180-247

Sequence: 1 SLNYKKMLILSLGTGTSEF.....LSISVATRLAQKDPAFASIR 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 1865 | 100.0 | 366 | 4 AAG99308 | AAG99308 Permutin |
| 2 | 1865 | 100.0 | 366 | 8 ADM93060 | ADM93060 Permutin |
| 3 | 1865 | 100.0 | 389 | 4 AAG99314 | AAG99314 Permutin |
| 4 | 1865 | 100.0 | 389 | 8 ADM93072 | ADM93072 Permutin |
| 5 | 1769 | 94.9 | 389 | 4 AAG99315 | AAG99315 Permutin |
| 6 | 1769 | 94.9 | 389 | 8 ADM93074 | ADM93074 Permutin |
| 7 | 1753 | 94.0 | 366 | 4 AAG99311 | AAG99311 Permutin |
| 8 | 1753 | 94.0 | 366 | 8 ADM93066 | ADM93066 Permutin |
| 9 | 1645 | 88.2 | 366 | 4 AAG99309 | AAG99309 Permutin |
| 10 | 1645 | 88.2 | 366 | 8 ADM93062 | ADM93062 Permutin |
| 11 | 1544 | 82.8 | 366 | 4 AAG99310 | AAG99310 Permutin |
| 12 | 1544 | 82.8 | 366 | 8 ADM93064 | ADM93064 Permutin |
| 13 | 1480 | 79.4 | 366 | 4 AAG99312 | AAG99312 Permutin |
| 14 | 1480 | 79.4 | 366 | 8 ADM93068 | ADM93068 Permutin |
| 15 | 1480 | 79.4 | 366 | 4 AAG993081 | AAG993081 Permutin |
| 16 | 1480 | 79.4 | 366 | 8 ADM93080 | ADM93080 Permutin |
| 17 | 1480 | 79.4 | 366 | 4 AAG99325 | AAG99325 Permutin |
| 18 | 1480 | 79.4 | 366 | 8 ADM93044 | ADM93044 Permutin |
| 19 | 1480 | 79.4 | 366 | 4 AAG99313 | AAG99313 Permutin |
| 20 | 1480 | 79.4 | 366 | 8 ADM93079 | ADM93079 Permutin |
| 21 | 1480 | 79.4 | 366 | 4 AAG993070 | AAG993070 Permutin |
| 22 | 1480 | 79.4 | 366 | 8 ADM93040 | ADM93040 Permutin |
| 23 | 1480 | 79.4 | 366 | 4 AAG993078 | ADM93078 Permutin |
| 24 | 1480 | 79.4 | 366 | 8 ADM93078 | ADM93078 Permutin |
| 25 | 1480 | 79.4 | 366 | 4 AAG993080 | ADM93080 Permutin |

| | | | | | |
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| 26 | 1030.5 | 55.3 | 383 | 2 AAW74512 | AAW74512 Amino aci |
| 27 | 1019 | 54.6 | 386 | 4 AAG99319 | AAG99319 Patatin i |
| 28 | 1019 | 54.6 | 386 | 8 ADM93045 | ADM93045 Patatin i |
| 29 | 1017 | 54.5 | 386 | 4 AAG99318 | AAG99318 Patatin i |
| 30 | 1017 | 54.5 | 386 | 8 ADM93044 | ADM93044 Patatin i |
| 31 | 1014 | 54.4 | 381 | 2 AAW74511 | AAW74511 Amino aci |
| 32 | 1014 | 54.4 | 381 | 2 AAW74511 | AAW74511 Amino aci |
| 33 | 1014 | 54.4 | 386 | 4 AAG99322 | AAG99322 Patatin i |
| 34 | 1014 | 54.4 | 386 | 8 ADM93043 | ADM93043 Patatin i |
| 35 | 1013 | 54.3 | 364 | 4 AAG99321 | AAG99321 Patatin i |
| 36 | 1013 | 54.3 | 364 | 8 ADM93042 | ADM93042 Patatin i |
| 37 | 1001.5 | 53.7 | 365 | 4 AAG99320 | AAG99320 Patatin i |
| 38 | 1001.5 | 53.7 | 365 | 8 ADM93041 | ADM93041 Patatin i |
| 39 | 618.5 | 33.2 | 400 | 3 AAG20550 | AAG20550 Arabidops |
| 40 | 618.5 | 33.2 | 400 | 3 AAG50025 | AAG50025 Arabidops |
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| 43 | 614 | 32.9 | 414 | 3 AAG30649 | AAG30649 Arabidops |
| 44 | 613 | 32.9 | 420 | 5 AAM52549 | AAM52549 Nicotiana |
| 45 | 609.5 | 32.7 | 405 | 4 AAE02385 | AAE02385 Rice lipi |

ALIGNMENTS

RESULT 1

AAAG99308 standard; protein: 366 AA.

AAAG99308; 28-SEP-2001 (first entry)
Permutin protein #1.
Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
larva growth; lipid acyl hydrolase; insecticide.
Unidentified.
WO200149834-A2.
12-JUL-2001.
05-JAN-2001; 2001WO-US000342.
06-JAN-2000; 2000US-0174669P.
(MONS) MONSANTO CO.
Alibhai MF, Astwood JD, McWhorter CA, Sampson HA;
WPI; 2001-441874/47.
Modified potato patatin proteins with reduced antigenicity, useful as
insecticides for controlling e.g. round worm and root worm.
Claim 26; Page 183-184; 223pp; English.
The present invention relates to modified potato patatins that maintain
enzymatic and insecticidal activity but which have reduced allergenicity.
Groups (especially Tyr) which bind to anti-patatin antibodies were
identified and glycosylation sites involved in antibody binding were
removed via site directed mutagenesis. The patatins stunt the growth of
larvae so that maturation is prevented or delayed. The patatins also have
non-specific lipid acyl hydrolase activity. The modified patatins are
also useful for inhibiting the activity of corn round worms.
Dallergenic protein can be used as insecticides, as nutritional
supplements and as immunising agents. The present sequence was used to
illustrate the present invention
Sequence 366 AA;

Query Match 100.0%; Score 1865; DB 4; Length 366;
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
 CC as nutritional supplements, and in immunotherapy protocols. The present
 CC sequence represents the amino acid sequence of permutein.

XX Sequence 366 AA:

1 SLNYKKLLSLGTTSEFDKTYTAKEAATWTAHVHMLVIQKMTDAASSYMTDYLYSTA 60
 1 SLNYKKLLSLGTTSEFDKTYTAKEAATWTAHVHMLVIQKMTDAASSYMTDYLYSTA 60
 61 FQALDSKNYLRVQENALTGTTTMDASEANMELLVQGENILKKPVSEDNPEYEEAL 120
 61 FQALDSKNYLRVQENALTGTTTMDASEANMELLVQGENILKKPVSEDNPEYEEAL 120
 121 KRPAKLSDRKLRANKASYGPGQLGEMVTYVLSIDGGIRGIIIPATLLEFLBQQLQEMDN 180
 121 KRPAKLSDRKLRANKASYGPGQLGEMVTYVLSIDGGIRGIIIPATLLEFLBQQLQEMDN 180
 181 NADARLADYFDVIGSTGGLTPTAMISTPENNRPPAAKEIYFYEFGPOIFNPSGOI 240
 181 NADARLADYFDVIGSTGGLTPTAMISTPENNRPPAAKEIYFYEFGPOIFNPSGOI 240
 241 LGPKYDGKYLMOYLQEKLGSTRVHQALTEVVISFPIKTKNPVIFPKSNLANSPELDAM 300
 241 LGPKYDGKYLMOYLQEKLGSTRVHQALTEVVISFPIKTKNPVIFPKSNLANSPELDAM 300
 301 YDISYSTAAAPTYPPHYFVTNTSNGDEYEFNLVDGAVATVADPALISVATRLAQKP 360
 301 YDISYSTAAAPTYPPHYFVTNTSNGDEYEFNLVDGAVATVADPALISVATRLAQKP 360
 361 APASIR 366
 361 APASIR 366

RESULT 2

ID ADM93060 standard; protein; 366 AA.

ADM93060;

03-JUN-2004 (first entry)

permutein protein #1.

lipid acyl hydrolase; corn rootworm; insect infestation; plant;
 insect control; nutritional supplement; ds; permutein.

Synthetic.

US6657046-B1.

02-DEC-2003.

05-JAN-2001; 2001US-00755274.

06-JAN-2000; 2000US-0174669P.

21-JUL-2000; 2000US-0219912P.

(MONS) MONSANTO TECHNOLOGY LLC.

Alibhai MF, Rydel TJ;

WPI; 2004-058368/06.

N-PSDB; ADM93059.

New lipid acyl hydrolase proteins, useful for inhibiting insect
 infestation of a plant or plant part, for controlling insects, as
 nutritional supplements, or in immunotherapy protocols.

Example 6; SEQ ID NO 21; 73pp; English.

The invention relates to an isolated peptide exhibiting lipid acyl
 hydrolase activity and corn rootworm insect inhibitory bioactivity. The
 lipid acyl hydrolase peptide is useful for inhibiting insect infestation

Query Match 100.0%; Score 1865; DB 8; Length 366;
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
 CC as nutritional supplements, and in immunotherapy protocols. The present
 CC sequence represents the amino acid sequence of permutein.

XX Sequence 366 AA:

1 SLNYKKLLSLGTTSEFDKTYTAKEAATWTAHVHMLVIQKMTDAASSYMTDYLYSTA 60
 1 SLNYKKLLSLGTTSEFDKTYTAKEAATWTAHVHMLVIQKMTDAASSYMTDYLYSTA 60
 61 FQALDSKNYLRVQENALTGTTTMDASEANMELLVQGENILKKPVSEDNPEYEEAL 120
 61 FQALDSKNYLRVQENALTGTTTMDASEANMELLVQGENILKKPVSEDNPEYEEAL 120
 121 KRPAKLSDRKLRANKASYGPGQLGEMVTYVLSIDGGIRGIIIPATLLEFLBQQLQEMDN 180
 121 KRPAKLSDRKLRANKASYGPGQLGEMVTYVLSIDGGIRGIIIPATLLEFLBQQLQEMDN 180
 181 NADARLADYFDVIGSTGGLTPTAMISTPENNRPPAAKEIYFYEFGPOIFNPSGOI 240
 181 NADARLADYFDVIGSTGGLTPTAMISTPENNRPPAAKEIYFYEFGPOIFNPSGOI 240
 241 LGPKYDGKYLMOYLQEKLGSTRVHQALTEVVISFPIKTKNPVIFPKSNLANSPELDAM 300
 241 LGPKYDGKYLMOYLQEKLGSTRVHQALTEVVISFPIKTKNPVIFPKSNLANSPELDAM 300
 301 YDISYSTAAAPTYPPHYFVTNTSNGDEYEFNLVDGAVATVADPALISVATRLAQKP 360
 301 YDISYSTAAAPTYPPHYFVTNTSNGDEYEFNLVDGAVATVADPALISVATRLAQKP 360
 361 APASIR 366
 361 APASIR 366

RESULT 3

ID AAG99314 standard; protein; 389 AA.

AAG99314;

28-SEP-2001 (first entry)

permutein protein #7.

Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
 larva growth; lipid acyl hydrolase; insecticide.

Unidentified.

WO200149834-A2.

12-JUL-2001.

05-JAN-2001; 2001WO-US000342.

06-JAN-2000; 2000US-0174669P.

(MONS) MONSANTO CO.

Alibhai MF, Actwood JD, Mcwhorter CA, Sampson HA;

WPI; 2001-441874/47.

Modified potato patatin proteins with reduced antigenicity, useful as
 insecticides for controlling e.g. round worm and root worm.

Claim 60; Page 198-199; 223pp; English.

CC The present invention relates to modified potato patatins that maintain
 CC enzymatic and insecticidal activity but which have reduced allergenicity.
 CC Groups (especially Tyr) which bind to anti-patatin antibodies were
 CC identified and glycosylation sites involved in antibody binding were
 CC removed via site directed mutagenesis. The patatins stunt the growth of
 CC larvae so that maturation is prevented or delayed. The patatins also have
 CC non-specific lipid acyl hydrolase activity. The modified patatins are
 CC also useful for inhibiting the activity of corn root worms.
 CC Deallergensd protein can be used as insecticides, as nutritional
 CC supplements and as immunising agents. The present sequence was used to
 CC illustrate the present invention

XX Sequence 389 AA;

Query Match 100.0%; Score 1865; DB 4; Length 389;
 Best Local Similarity 100.0%; Pred. No.7.5e-163;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAHVHMLVIOKMTDAASSYMTDYVYSTA 60
 DB 24 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAHVHMLVIOKMTDAASSYMTDYVYSTA 83
 QY 61 FOALDSKNNTLRVQENALTGTTTMDASANNELLVQVGENILKKPVSEDNPEYREAL 120
 DB 84 FOALDSKNNTLRVQENALTGTTTMDASANNELLVQVGENILKKPVSEDNPEYREAL 143
 QY 121 KRPAKLISDRKKLRANKASVGPOLGEMTVVLSIDGGIRGIIIPATLLEFLGQLOEMDN 180
 DB 144 KRPAKLISDRKKLRANKASVGPOLGEMTVVLSIDGGIRGIIIPATLLEFLGQLOEMDN 203
 QY 181 NADARLADYDVIGTSTGILTLAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 240
 DB 204 NADARLADYDVIGTSTGILTLAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 263
 QY 241 LGRKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 300
 DB 264 LGRKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 323
 QY 301 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 360
 DB 324 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 383
 QY 361 AFASIR 366
 DB 384 AFASIR 389

RESULT 4

ADM93072 standard; protein; 389 AA.

XX ADM93072;

XX 03-JUN-2004 (first entry)

XX Permutin protein #7.

XX lipid acyl hydrolase; corn rootworm; insect infestation; plant;
 KW insect control; nutritional supplement; ds; permutin.

XX Synthetic.

XX US6657046-B1.

XX 02-DEC-2003.

XX 05-JAN-2001; 2001US-00755274.

XX 06-JAN-2000; 2000US-0174669P.

XX 21-JUL-2000; 2000US-0219912P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

PI Aibhai MF, Rydel TJ;

XX WPI; 2004-056368/06.

DR N-PSDB; ADM93071.

XX New lipid acyl hydrolase proteins, useful for inhibiting insect
 PT infestation of a plant or plant part, for controlling insects, as
 PT nutritional supplements, or in immunotherapy protocols.

XX Example 6; SEQ ID NO 33; 73pp; English.

XX The invention relates to an isolated peptide exhibiting lipid acyl
 CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The
 CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation
 CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
 CC as nutritional supplements, and in immunotherapy protocols. The present
 CC sequence represents the amino acid sequence of permutin.

XX Sequence 389 AA;

Query Match 100.0%; Score 1865; DB 8; Length 389;
 Best Local Similarity 100.0%; Pred. No.7.5e-163;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAHVHMLVIOKMTDAASSYMTDYVYSTA 60
 DB 24 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAHVHMLVIOKMTDAASSYMTDYVYSTA 83
 QY 61 FOALDSKNNTLRVQENALTGTTTMDASANNELLVQVGENILKKPVSEDNPEYREAL 120
 DB 84 FOALDSKNNTLRVQENALTGTTTMDASANNELLVQVGENILKKPVSEDNPEYREAL 143
 QY 121 KRPAKLISDRKKLRANKASVGPOLGEMTVVLSIDGGIRGIIIPATLLEFLGQLOEMDN 180
 DB 144 KRPAKLISDRKKLRANKASVGPOLGEMTVVLSIDGGIRGIIIPATLLEFLGQLOEMDN 203
 QY 181 NADARLADYDVIGTSTGILTLAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 240
 DB 204 NADARLADYDVIGTSTGILTLAMISTPENNRPFPAAKEIVPFYEHGPOIFNPSGOI 263
 QY 241 LGRKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 300
 DB 264 LGRKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 323
 QY 301 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 360
 DB 324 YDISYSTAAAPTYPPHYFVTNTSNGDEVEFNLDGAVATVADPALISVATRLAQKP 383
 QY 361 AFASIR 366
 DB 384 AFASIR 389

RESULT 5

AA699315 standard; protein; 389 AA.

XX AA699315;

XX 28-SEP-2001 (first entry)

XX Permutin protein #8.

XX Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
 KW larva growth; lipid acyl hydrolase; insecticide.

XX Unidentified.

XX WO200149834-A2.

XX 12-JUL-2001.

XX 05-JAN-2001; 2001WO-US000342.

XX MO200149834-A2.
PN
XX 12-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US000342.
XX
XX 06-JAN-2000; 2000US-0174669P.
XX
XX (MONS) MONSANTO CO.
XX
XX Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA;
PI
XX MPI; 2001-441874/47.
XX
XX Modified potato patatin proteins with reduced antigenicity, useful as
PT insecticides for controlling e.g. round worm and root worm.
XX
XX Claim 27; Page 190-192; 223pp; English.
XX
XX The present invention relates to modified potato patatins that maintain
CC enzymatic and insecticidal activity but which have reduced allergenicity.
CC Groups (especially Tyr) which bind to anti-patatin antibodies were
CC identified and glycosylation sites involved in antibody binding were
CC removed via site directed mutagenesis. The patatins stunt the growth of
CC larvae so that maturation is prevented or delayed. The patatins also have
CC larva so that maturation is prevented or delayed. The patatins also have
CC also useful for inhibiting the activity of corn round worms.
CC Dehydrated protein can be used as insecticides, as nutritional
CC supplements and as immunising agents. The present sequence was used to
CC illustrate the present invention
XX
XX Sequence 366 AA;

Query Match 94.0%; Score 1753; DB 4; Length 366;
Best Local Similarity 99.7%; Pred. No. 1.4e-152;
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 TTTAKAAATWTAHVMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGQENALTGTT 82
DB 1 TTTAKAAATWTAHVMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGQENALTGTT 60
QY 83 TEMDDASSEANMELLVGVGENLLKKPVSEDPETYEALKRFAKLSDRKLDRKANKASYGP 142
DB 61 TEMDDASSEANMELLVGVGENLLKKPVSEDPETYEALKRFAKLSDRKLDRKANKASYGP 120
QY 143 GOLGEMVTVLSTIDGGGIRGIIIPATILFELEGQLQEMDNNDARLADYFDVIGSTGGL 202
DB 121 GOLGEMVTVLSTIDGGGIRGIIIPATILFELEGQLQEMDNNDARLADYFDVIGSTGGL 180
QY 203 TAMISTPNENNRPFPAAKEIVPEYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 262
DB 181 TAMISTPNENNRPFPAAKEIVPEYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 240
QY 263 VHQALTEVVISSEDITKPKVITFTKSNLANSPELDKMDISYSTAAAPYFPPHYFTN 322
DB 241 VHQALTEVVISSEDITKPKVITFTKSNLANSPELDKMDISYSTAAAPYFPPHYFTN 300
QY 323 TNSGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 366
DB 301 TNSGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 344

RESULT 8
ADM93066
ID ADM93066 standard; protein; 366 AA.
XX
XX ADM93066;
XX
XX 03-JUN-2004 (first entry)
XX
XX Permutectin protein #4.
XX

KM lipid acyl hydrolase; corn rootworm; insect infestation; plant;
KM insect control; nutritional supplement; de; permutectin.
XX
XX Synthetic.
XX
XX US6657046-B1.
XX
XX 02-DEC-2003.
XX
XX 05-JAN-2001; 2001US-00755274.
XX
XX 06-JAN-2000; 2000US-0174669P.
XX
XX 21-JUL-2000; 2000US-0219912P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
XX Alibhai MF, Rydel TJ;
PI
XX MPI; 2004-058368/06.
XX
XX N-PSDB; ADM93065.
XX
XX New lipid acyl hydrolase proteins, useful for inhibiting insect
PT infestation of a plant or plant part, for controlling insects, as
PT nutritional supplements, or in immunotherapy protocols.
XX
XX Example 6; SEQ ID NO 27; 73pp; English.
XX
XX The invention relates to an isolated peptide exhibiting lipid acyl
CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The
CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation
CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
CC as nutritional supplements, and in immunotherapy protocols. The present
CC sequence represents the amino acid sequence of permutectin.
XX
XX Sequence 366 AA;

Query Match 94.0%; Score 1753; DB 8; Length 366;
Best Local Similarity 99.7%; Pred. No. 1.4e-152;
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 TTTAKAAATWTAHVMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGQENALTGTT 82
DB 1 TTTAKAAATWTAHVMVLVIQKMTDAASVWTDYLLSTAFOALDSKNNYLKVGQENALTGTT 60
QY 83 TEMDDASSEANMELLVGVGENLLKKPVSEDPETYEALKRFAKLSDRKLDRKANKASYGP 142
DB 61 TEMDDASSEANMELLVGVGENLLKKPVSEDPETYEALKRFAKLSDRKLDRKANKASYGP 120
QY 143 GOLGEMVTVLSTIDGGGIRGIIIPATILFELEGQLQEMDNNDARLADYFDVIGSTGGL 202
DB 121 GOLGEMVTVLSTIDGGGIRGIIIPATILFELEGQLQEMDNNDARLADYFDVIGSTGGL 180
QY 203 TAMISTPNENNRPFPAAKEIVPEYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 262
DB 181 TAMISTPNENNRPFPAAKEIVPEYFEHGPQIFNPSCQILGPKYDGKYLQVLOEKLGETR 240
QY 263 VHQALTEVVISSEDITKPKVITFTKSNLANSPELDKMDISYSTAAAPYFPPHYFTN 322
DB 241 VHQALTEVVISSEDITKPKVITFTKSNLANSPELDKMDISYSTAAAPYFPPHYFTN 300
QY 323 TNSGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 366
DB 301 TNSGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 344

RESULT 9
AAG9309
ID AAG9309 standard; protein; 366 AA.
XX
XX AAG9309;
XX
XX 28-SEP-2001 (first entry)
XX

DE Permutin protein #2.
XX Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
KW larva growth; lipid acyl hydrolase; insecticide.
XX Unidentified.
OS
XX WO000149834-A2.
PN
XX 12-JUL-2001.
PD
XX 05-JAN-2001, 2001MO-US000342.
PF
XX 06-JAN-2000, 2000US-0174669P.
PR
XX (MONS) MONSANTO CO.
XX
XX Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA;
PI WPI; 2001-441874/47.
XX
XX Modified potato patatin proteins with reduced antigenicity, useful as
PT insecticides for controlling e.g. round worm and root worm.
XX
XX Claim 60; Page 186-187; 223pp; English.
PS
XX
XX The present invention relates to modified potato patatins that maintain
CC enzymatic and insecticidal activity but which have reduced allergenicity.
CC Groups (especially Tyr) which bind to anti-patatin antibodies were
CC identified and glycosylation sites involved in antibody binding were
CC removed via site directed mutagenesis. The patatins stunt the growth of
CC larvae so that maturation is prevented or delayed. The patatins also have
CC non-specific lipid acyl hydrolase activity. The modified patatins are
CC also useful for inhibiting the activity of corn round worms.
CC Deallergised protein can be used as insecticides, as nutritional
CC supplements and as immunising agents. The present sequence was used to
CC illustrate the present invention
XX
XX Sequence 366 AA;
SQ

Query Match 88.2%; Score 1645; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKMLLSLGTSTSEFDKTYTAKAATWAVHMLVIQMTDAASSYMTDYLLSTA 60
DB 46 SLNYKMLLSLGTSTSEFDKTYTAKAATWAVHMLVIQMTDAASSYMTDYLLSTA 105
QY 61 FQALDSKNNYLKRVQENALTGTTTMDASEANMELLVQGENLLKKPVSEDNPEYEEAL 120
DB 106 FQALDSKNNYLKRVQENALTGTTTMDASEANMELLVQGENLLKKPVSEDNPEYEEAL 165
QY 121 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 180
DB 166 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 225
QY 181 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 240
DB 226 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 285
QY 241 LGRKYDGKTYLMQVLOEKLGETRVHQALETVEVLISSFDIKTKNPVIFTKSNLANSPELDAM 300
DB 286 LGRKYDGKTYLMQVLOEKLGETRVHQALETVEVLISSFDIKTKNPVIFTKSNLANSPELDAM 345
QY 301 YDISYSTAAAPTYFPPHYFVT 321
DB 346 YDISYSTAAAPTYFPPHYFVT 366

RESULT 10
ADM93062
ID ADM93062 standard; protein; 366 AA.
XX

AC ADM93062;
XX
XX 03-JUN-2004 (first entry)
DT
XX Permutin protein #2.
DE
XX
XX lipid acyl hydrolase; corn rootworm; insect infestation; plant;
KW insect control; nutritional supplement; ds; permutin.
XX
XX Synthetic.
OS
XX
XX US6657046-B1.
PN
XX 02-DEC-2003.
PD
XX 05-JAN-2001, 2001US-00755274.
PF
XX 06-JAN-2000, 2000US-0174669P.
PR 21-JUL-2000, 2000US-0219912P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
XX Alibhai MF, Rydel TJ;
PI WPI; 2004-058368/06.
XX
XX N-PSDB; ADM93061.
DR
XX
XX New lipid acyl hydrolase proteins, useful for inhibiting insect
PT infestation of a plant or plant part, for controlling insects, as
PT nutritional supplements, or in immunotherapy protocols.
XX
XX Example 6; SEQ ID NO 23; 73pp; English.
PS
XX
XX The invention relates to an isolated peptide exhibiting lipid acyl
CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The
CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation
CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
CC as nutritional supplements, and in immunotherapy protocols. The present
CC sequence represents the amino acid sequence of permutin.
XX
XX Sequence 366 AA;
SQ

Query Match 88.2%; Score 1645; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKMLLSLGTSTSEFDKTYTAKAATWAVHMLVIQMTDAASSYMTDYLLSTA 60
DB 46 SLNYKMLLSLGTSTSEFDKTYTAKAATWAVHMLVIQMTDAASSYMTDYLLSTA 105
QY 61 FQALDSKNNYLKRVQENALTGTTTMDASEANMELLVQGENLLKKPVSEDNPEYEEAL 120
DB 106 FQALDSKNNYLKRVQENALTGTTTMDASEANMELLVQGENLLKKPVSEDNPEYEEAL 165
QY 121 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 180
DB 166 KRPALKLSRKKLRANKASVGPQLGEMTVLSIDGGIRGIIIPATILFLEBQLOEMDN 225
QY 181 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 240
DB 226 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIIVPFYFEGHPOIFNPSGOI 285
QY 241 LGRKYDGKTYLMQVLOEKLGETRVHQALETVEVLISSFDIKTKNPVIFTKSNLANSPELDAM 300
DB 286 LGRKYDGKTYLMQVLOEKLGETRVHQALETVEVLISSFDIKTKNPVIFTKSNLANSPELDAM 345
QY 301 YDISYSTAAAPTYFPPHYFVT 321
DB 346 YDISYSTAAAPTYFPPHYFVT 366

RESULT 11
AAG9310

ID AAG9310 standard; protein; 366 AA.
AC AAG9310;
XX
XX 28-SEP-2001 (first entry)
DT
XX Permutin protein #3.
DE
XX Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;
KM larva growth; lipid acyl hydrolase; insecticide.
XX
XX Unidentified.
OS
XX MO200149834-A2.
PN
XX 12-JUL-2001.
PD
XX 05-JAN-2001; 2001WO-US000342.
PF
XX 06-JAN-2000; 2000US-0174669P.
PR
XX (MONS) MONSANTO CO.
PA
XX Alibhai MF, Astwood JD, Mcwherter CA, Sampson HA;
PI
XX WPI; 2001-441874/47.
DR
XX Modified potato patatin proteins with reduced antigenicity, useful as
PT insecticides for controlling e.g. round worm and root worm.
XX
XX Claim 60; Page 188-189; 223pp; English.
XX
XX The present invention relates to modified potato patatins that maintain
CC enzymatic and insecticidal activity but which have reduced allergenicity.
CC Groups (especially Ty) which bind to anti-patatin antibodies were
CC identified and glycosylation sites involved in antibody binding were
CC removed via site directed mutagenesis. The patatins stunt the growth of
CC larvae so that maturation is prevented or delayed. The patatins also have
CC non-specific lipid acyl hydrolase activity. The modified patatins are
CC also useful for inhibiting the activity of corn round worms.
CC Deallerghed protein can be used as insecticides, as nutritional
CC supplements and as immunising agents. The present sequence was used to
CC illustrate the present invention
CC
XX
XX Sequence 366 AA;
SQ

Query Match 82.8%; Score 1544; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 2.6e-133;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOQWTDAAASYMTDYLYSTA 60
DB 64 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOQWTDAAASYMTDYLYSTA 123
QY 61 FOALDSKNYVLRVOENALGTTEMDASANNELLVQVGENLLKKPVSDNBEYEEAL 120
DB 124 FOALDSKNYVLRVOENALGTTEMDASANNELLVQVGENLLKKPVSDNBEYEEAL 183
QY 121 KRFPAKLSRKKLRANKASYGPGOLGEMVTVLSIDGGGIRGIIIPATILFELEGOLQEMDN 180
DB 184 KRFPAKLSRKKLRANKASYGPGOLGEMVTVLSIDGGGIRGIIIPATILFELEGOLQEMDN 243
QY 181 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEGHGPQIFNPSGQI 240
DB 244 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEGHGPQIFNPSGQI 303
QY 241 LGPKYDGKYLMOVLQERLGETRVHQAALTEVYISSFDIKTKNPVIFTKSNLANSPELDAM 300
DB 304 LGPKYDGKYLMOVLQERLGETRVHQAALTEVYISSFDIKTKNPVIFTKSNLANSPELDAM 363
QY 301 YDI 303
DB 364 YDI 366

RESULT 12
ADM93064
ID ADM93064 standard; protein; 366 AA.
XX
XX ADM93064;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX Permutin protein #3.
DE
XX
XX lipid acyl hydrolase; corn rootworm; insect infestation; plant;
KM insect control; nutritional supplement; de; permutin.
XX
XX Synthetic.
OS
XX US6657046-B1.
PN
XX
XX 02-DEC-2003.
PD
XX
XX 05-JAN-2001; 2001US-00755274.
PF
XX 06-JAN-2000; 2000US-0174669P.
PR
XX 21-JUL-2000; 2000US-0219912P.
PR
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA
XX Alibhai MF, Rydel TJ;
PI
XX WPI; 2004-058368/06.
DR
XX N-FSDB; ADM93063.
XX
XX New lipid acyl hydrolase proteins, useful for inhibiting insect
PT infestation of a plant or plant part, for controlling insects, as
PT nutritional supplements, or in immunotherapy protocols.
XX
XX Example 6; SEQ ID NO 25; 73pp; English.
PS
XX The invention relates to an isolated peptide exhibiting lipid acyl
CC hydrolase activity and corn rootworm insect inhibitory bioactivity. The
CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation
CC of a plant or plant part, for controlling insects (e.g. corn rootworm),
CC as nutritional supplements, and in immunotherapy protocols. The present
CC sequence represents the amino acid sequence of permutin.
CC
XX
XX Sequence 366 AA;
SQ

Query Match 82.8%; Score 1544; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 2.6e-133;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOQWTDAAASYMTDYLYSTA 60
DB 64 SLNYKKMLLSLGTGTTSEFDKTYTAKEATWTAHVHMLVIOQWTDAAASYMTDYLYSTA 123
QY 61 FOALDSKNYVLRVOENALGTTEMDASANNELLVQVGENLLKKPVSDNBEYEEAL 120
DB 124 FOALDSKNYVLRVOENALGTTEMDASANNELLVQVGENLLKKPVSDNBEYEEAL 183
QY 121 KRFPAKLSRKKLRANKASYGPGOLGEMVTVLSIDGGGIRGIIIPATILFELEGOLQEMDN 180
DB 184 KRFPAKLSRKKLRANKASYGPGOLGEMVTVLSIDGGGIRGIIIPATILFELEGOLQEMDN 243
QY 181 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEGHGPQIFNPSGQI 240
DB 244 NADARLADYFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEGHGPQIFNPSGQI 303
QY 241 LGPKYDGKYLMOVLQERLGETRVHQAALTEVYISSFDIKTKNPVIFTKSNLANSPELDAM 300
DB 304 LGPKYDGKYLMOVLQERLGETRVHQAALTEVYISSFDIKTKNPVIFTKSNLANSPELDAM 363
QY 301 YDI 303

DB 364 YDI 366

RESULT 13

ADMG9312 standard; protein; 366 AA.

AC AAG9312;

DT 28-SEP-2001 (first entry)

DE Permutin protein #5.

KM Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity; larva growth; lipid acyl hydrolase; insecticide.

OS Unidentified.

PN WO200149834-A2.

PD 12-JUL-2001.

PF 05-JAN-2001; 2001MO-US000342.

PR 06-JAN-2000; 2000US-0174669P.

PA (MONS) MONSANTO CO.

PI Alibhai MF, Aetwood JD, Mcwherter CA, Sampson HA;

DR WPI; 2001-441874/47.

PT Modified potato patatin proteins with reduced antigenicity, useful as insecticides for controlling e.g. round worm and root worm.

PS Claim 60; Page 193-194; 223pp; English.

CC The present invention relates to modified potato patatins that maintain enzymatic and insecticidal activity but which have reduced allergenicity. CC Groups (especially Tyr) which bind to anti-patatin antibodies were identified and glycosylation sites involved in antibody binding were removed via site directed mutagenesis. The patatins stunt the growth of larvae so that maturation is prevented or delayed. The patatins also have CC non-specific lipid acyl hydrolase activity. The modified patatins are CC also useful for inhibiting the activity of corn round worms. CC Deallerenised protein can be used as insecticides, as nutritional CC supplements and as immunising agents. The present sequence was used to CC illustrate the present invention

SO Sequence 366 AA;

Query Match 79.4%; Score 1480; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 2.1e-127; Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 76 NALTGTTTMDSDSEANMELLVOVGENLKKPVSEDPETYEALRFAKLSDRKKLRA 135

DB 1 NALTGTTTMDSDSEANMELLVOVGENLKKPVSEDPETYEALRFAKLSDRKKLRA 60

DB 136 NKASVPGQIGENVTVLSDGGIRGIIPATILFLEGGLOEMDNADARLADYFVIGG 195

DB 61 NKASVPGQIGENVTVLSDGGIRGIIPATILFLEGGLOEMDNADARLADYFVIGG 120

DB 196 TSTGGLTMTMISTPNENNRPPAAKEIVPFYFHHGQIFNPSQILGPKYDGYLMQVLA 255

DB 121 TSTGGLTMTMISTPNENNRPPAAKEIVPFYFHHGQIFNPSQILGPKYDGYLMQVLA 180

DB 256 EKIGETRVHQAALTEVVISFSDIKTKNPVIFTKSNLANSELDKAMDISTSYAAATYFP 315

DB 181 EKIGETRVHQAALTEVVISFSDIKTKNPVIFTKSNLANSELDKAMDISTSYAAATYFP 240

DB 316 PHYFVNTNSNGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 366

DB 241 PHYFVNTNSNGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 291

RESULT 14

ADMG3068 standard; protein; 366 AA.

AC ADM93068;

DT 03-JUN-2004 (first entry)

DE Permutin protein #5.

KM lipid acyl hydrolase; corn rootworm; insect infestation; plant; insect control; nutritional supplement; ds; permutin.

OS Synthetic.

PN US6657046-B1.

PD 02-DEC-2003.

PF 05-JAN-2001; 2001US-00755274.

PR 06-JAN-2000; 2000US-0174669P.

PA 21-JUL-2000; 2000US-0219912P.

PI (MONS) MONSANTO TECHNOLOGY LLC.

PI Alibhai MF, Rydel TU;

DR WPI; 2004-058368/06.

DR N-PSDB; ADM93067.

PT New lipid acyl hydrolase proteins, useful for inhibiting insect infestation of a plant or plant part, for controlling insects, as

PT nutritional supplements, or in immunotherapy protocols.

PS

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CC The invention relates to an isolated peptide exhibiting lipid acyl hydrolase activity and corn rootworm insect inhibitory bioactivity. The CC lipid acyl hydrolase peptide is useful for inhibiting insect infestation of a plant or plant part, for controlling insects (e.g. corn rootworm), CC as nutritional supplements, and in immunotherapy protocols. The present CC sequence represents the amino acid sequence of permutin.

SO Sequence 366 AA;

Query Match 79.4%; Score 1480; DB 8; Length 366;

Best Local Similarity 100.0%; Pred. No. 2.1e-127; Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 76 NALTGTTTMDSDSEANMELLVOVGENLKKPVSEDPETYEALRFAKLSDRKKLRA 135

DB 1 NALTGTTTMDSDSEANMELLVOVGENLKKPVSEDPETYEALRFAKLSDRKKLRA 60

DB 136 NKASVPGQIGENVTVLSDGGIRGIIPATILFLEGGLOEMDNADARLADYFVIGG 195

DB 61 NKASVPGQIGENVTVLSDGGIRGIIPATILFLEGGLOEMDNADARLADYFVIGG 120

DB 196 TSTGGLTMTMISTPNENNRPPAAKEIVPFYFHHGQIFNPSQILGPKYDGYLMQVLA 255

DB 121 TSTGGLTMTMISTPNENNRPPAAKEIVPFYFHHGQIFNPSQILGPKYDGYLMQVLA 180

DB 256 EKIGETRVHQAALTEVVISFSDIKTKNPVIFTKSNLANSELDKAMDISTSYAAATYFP 315

DB 181 EKIGETRVHQAALTEVVISFSDIKTKNPVIFTKSNLANSELDKAMDISTSYAAATYFP 240

DB 316 PHYFVNTNSNGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 366

DB 241 PHYFVNTNSNGDEYEFNLVDGAATVADPALLSISVATRLAQDPAFASIR 291

RESULT 15

AAG99081

ID AAG99081 standard; protein; 367 AA.

AC AAG99081;

XX

XX

DT 28-SEP-2001 (first entry)

XX

XX

DE Pre-cleavage patatin protein #2.

XX

KW Insecticidal; immunosuppressive; potato; patatin; enzyme; allergenicity;

XX larva growth; lipid acyl hydrolase; insecticide.

XX

OS Unidentified.

XX

PN WO200149834-A2.

XX

XX

PD 12-JUL-2001.

XX

PF 05-JAN-2001; 2001WO-US000342.

XX

PR 06-JAN-2000; 2000US-0174669P.

XX

(MONS) MONSANTO CO.

XX

PI Alibhai MF, Astwood JD, McWherter CA, Sampson HA;

XX

DR WPI; 2001-441874/47.

XX

XX

PT Modified potato patatin proteins with reduced antigenicity, useful as

XX

PS insecticides for controlling e.g. round worm and root worm.

XX

Claim 1; Page 138-139; 223pp; English.

XX

The present invention relates to modified potato patatins that maintain

XX

enzymatic and insecticidal activity but which have reduced allergenicity.

XX

Groups (especially Tyr) which bind to anti-patatin antibodies were

XX

identified and glycosylation sites involved in antibody binding were

XX

removed via site directed mutagenesis. The patatins stunt the growth of

XX

larvae so that maturation is prevented or delayed. The patatins also have

XX

non-specific lipid acyl hydrolase activity. The modified patatins are

XX

also useful for inhibiting the activity of corn round worms.

XX

Deallergens protein can be used as insecticides, as nutritional

XX

supplements and as immunising agents. The present sequence was used to

XX

illustrate the present invention

XX

Sequence 367 AA;

SQ

Query Match 61.1%; Score 1139; DB 4; Length 367;

Best Local Similarity 100.0%; Pred. No. 5.7e-96;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

144 OLGEMVTIVSINDGGIRGIIPATILFLEGGLOEMDNNDARLADYFDVIGSTGGLT 203

5 QLGEMVTIVSINDGGIRGIIPATILFLEGGLOEMDNNDARLADYFDVIGSTGGLT 64

204 AMISTPENNNRPPAAKKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 263

65 AMISTPENNNRPPAAKKEIVPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLGSTRV 124

264 HQALTEVIVSSFDIKTKNKPVIFTKSNLANSPELDACKYDISYSTAAPTYFPFHYVTNT 323

125 HQALTEVIVSSFDIKTKNKPVIFTKSNLANSPELDACKYDISYSTAAPTYFPFHYVTNT 184

324 SNGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366

185 SNGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 227

Search completed: April 8, 2005, 07:38:50

Job time : 177 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 07:27:49 ; Search time 45 Seconds
(without alignments)
782.563 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNYKKMLLSLGTGTTSEF.....LSISVATRLAQKDPAFASIR 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1033 | 55.4 | 386 | 2 A26017 | patatin T5 precurs |
| 2 | 1033 | 55.4 | 386 | 2 S51596 | patatin precursor, |
| 3 | 1017 | 54.5 | 386 | 2 A29810 | patatin - potato |
| 4 | 1014 | 54.4 | 386 | 2 S05592 | patatin precursor |
| 5 | 1014 | 54.4 | 386 | 2 B26017 | patatin T58 precu |
| 6 | 1011 | 54.2 | 384 | 2 A24142 | patatin precursor |
| 7 | 1004 | 53.8 | 386 | 2 T07592 | patatin precursor |
| 8 | 1002 | 53.7 | 377 | 2 S05593 | patatin precursor |
| 9 | 778.5 | 42.9 | 390 | 2 T03841 | patatin homolog - |
| 10 | 614 | 32.9 | 410 | 2 H85437 | patatin-like prote |
| 11 | 612 | 32.8 | 410 | 2 T52294 | patatin-like prote |
| 12 | 575 | 30.8 | 414 | 2 G85437 | patatin-like prote |
| 13 | 569.5 | 30.5 | 407 | 2 T00989 | hypothetical prote |
| 14 | 560 | 30.0 | 428 | 2 F85437 | patatin-like prote |
| 15 | 507.5 | 27.2 | 405 | 2 T10260 | patatin-like prote |
| 16 | 462.5 | 24.8 | 388 | 2 T10765 | patatin-like latex |
| 17 | 454.5 | 24.4 | 388 | 2 T10763 | patatin-like latex |
| 18 | 450.5 | 24.2 | 388 | 2 T10770 | patatin-like latex |
| 19 | 288.5 | 15.5 | 390 | 2 AG2093 | patatin-like prote |
| 20 | 284.5 | 15.3 | 399 | 2 T02560 | hypothetical prote |
| 21 | 275.5 | 14.8 | 488 | 2 T06725 | hypothetical prote |
| 22 | 257.5 | 13.8 | 526 | 2 T08541 | hypothetical prote |
| 23 | 243 | 13.0 | 382 | 2 T82109 | hypothetical prote |
| 24 | 212 | 11.4 | 355 | 2 B82354 | patatin-related pr |
| 25 | 198 | 10.6 | 490 | 2 B97815 | patatin bi precurs |
| 26 | 189 | 10.1 | 1023 | 2 T26261 | hypothetical prote |
| 27 | 185.5 | 9.9 | 679 | 2 G71615 | phospholipase A2-1 |
| 28 | 177 | 9.5 | 494 | 2 D71655 | patatin bi precurs |
| 29 | 159 | 8.5 | 60 | 2 A23634 | patatin precursor |

| | | | | | |
|----|-------|-----|------|----------|--------------------|
| 30 | 148 | 7.9 | 56 | 2 S08631 | patatin PG13 - pot |
| 31 | 146.5 | 7.9 | 468 | 2 T33857 | hypothetical prote |
| 32 | 143.5 | 7.7 | 456 | 2 T24442 | hypothetical prote |
| 33 | 135 | 7.2 | 1265 | 2 T02131 | hypothetical prote |
| 34 | 134 | 7.2 | 851 | 2 T12503 | hypothetical prote |
| 35 | 128 | 6.9 | 782 | 2 UC7284 | phospholipase A2 (|
| 36 | 125.5 | 6.7 | 1071 | 2 T22327 | hypothetical prote |
| 37 | 117.5 | 6.3 | 431 | 2 D87608 | hypothetical prote |
| 38 | 113.5 | 6.1 | 447 | 2 AD0168 | probable ATPase pr |
| 39 | 113.5 | 6.1 | 826 | 2 T06036 | hypothetical prote |
| 40 | 109.5 | 5.9 | 1237 | 2 D71850 | probable outer mem |
| 41 | 109 | 5.8 | 320 | 2 F70034 | conserved hypochet |
| 42 | 109 | 5.8 | 1048 | 2 A70592 | hypothetical prote |
| 43 | 108 | 5.8 | 845 | 1 GLVK | beta-glucosidase (|
| 44 | 107.5 | 5.8 | 318 | 2 S24923 | REG protein - Bac |
| 45 | 107.5 | 5.8 | 901 | 2 S50987 | SOK1 protein - Yea |

ALIGNMENTS

RESULT 1

A26017 patatin T5 precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004

C/Accession: A26017

R/Rosahl, S.; Schmidt, R.; Scheil, J.; Willmitzer, L.

Mol. Gen. Genet. 203, 214-220, 1986

A/Title: Isolation and characterization of a gene from Solanum tuberosum encoding patatin

A/Reference number: A26017

A/Accession: A26017

A/Molecule type: DNA

A/Residues: 1-386 <ROS>

A/Cross-references: UNIPROT: P15478

C/Superfamily: patatin

Query Match 55.4%; Score 1033; DB 2; Length 386;

Best Local Similarity 90.1%; Pred. No. 2.9e-67;

Matches 200; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 145 | IGENVTLSIDGGIRGIRIPATILEPFLGQLQEMNNADARLADYDPVIGSTGGLLTA | 204 |
| Db | 25 | IGENVTLSIDGGIRKIIIPATILEPFLGQLQEDVNTDARLADYDPVIGSTGGLLTA | 84 |
| Qy | 205 | MISTPENNRPPAAKSIIVFFYEHGQIFNPSGQILGPKYDKYLMQVLOEKLGRTVH | 264 |
| Db | 85 | MITPENETNRPFAAKDIPVFYEHGPKIFQSSGSIIFPKYDKYLMQVLOEKLGRTVH | 144 |
| Qy | 265 | QALTEVVISFDIKTKNKEVFTKSNLANSPELDAXWDISYTRAAFTYPPHYFVNTS | 324 |
| Db | 145 | QALTEVAISSFDIKTKNKEVFTKSNLAKSPDLAKMDICYSYTRAAFTYPPHYFVNTS | 204 |
| Qy | 325 | NGDEYEPNLVDGAVATVADPALISISVATRLAQKDPAFASIR | 366 |
| Db | 205 | NGDKYEPNLVDGAVATVDDPALISISVATRLAQVDPKFAIK | 246 |

RESULT 2

S51596 patatin precursor, non-sucrose-inducible - Solanum brevifolius

C/Species: Solanum brevifolius

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S51596

R/Banfalvi, Z.; Kossyal, Z.; Barta, E.

Mol. Gen. Genet. 245, 517-522, 1994

A/Title: Solanum brevifolius possesses a non-sucrose-inducible patatin gene.

A/Reference number: S51596; MUID: 95107249; EMBL: 7808402

A/Accession: S51596

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-386 <BAN>

A/Cross-references: UNIPROT: Q42502; EMBL: U09331; NID: G563124; PID: AAA66198.1; PID: G56312

C/Superfamily: patatin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-386/Product: patatin #status predicted <MAT>

Query Match 55.4%; Score 1033; DB 2; Length 386;
Best Local Similarity 89.6%; Pred. No. 2,9e-67;
Matches 199; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 145 LGEMVTVLSDGGIRGIIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 204
DB 25 LGEMVTVLSDGGIRGIIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 84
QY 205 MISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGYLMQVLOEKLGETRV 264
DB 85 MITTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 144
QY 265 QALTEVAISSFDIKTKNKPVIPTKSNLANSPELDAMKMDICYSTAAAPTYFPFHVTNT 324
DB 145 QALTEVAISSFDIKTKNKPVIPTKSNLAKSPELDAMKMDICYSTAAAPTYFPFHVTNT 204
QY 325 NGDEYEFNLVDGAVATVADPALSLISVATRLAQKDPAPASIR 366
DB 205 NGDKYEFNLVDGAVATVGDPAALSLISVATRLAQVDPKFASSIK 246

RESULT 3

A29810
patatin - potato

C/Species: Solanum tuberosum (potato)

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C/Accession: A29810
R/Mignery, G.A.; Pliskaard, C.S.; Park, W.D.

Gene 62, 27-44, 1988

A/Title: Molecular characterization of the patatin multigene family of potato.

A/Reference number: A29810; MUID:88226014; PMID:3371664

A/Accession: A29810

A/Molecule type: DNA

A/Residues: 1-386 <MTG>

A/Cross-references: UNIPROT:P11768; GB:M18880; NID:G169499; PIDN:AAA3819.1; PID:G169500

C/Genetics:

A/Introns: 56/3; 117/2; 169/3; 224/3; 320/3; 368/2

C/Superfamily: patatin

Query Match 54.5%; Score 1017; DB 2; Length 386;
Best Local Similarity 87.9%; Pred. No. 4.2e-66;
Matches 196; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMVTVLSDGGIRGIIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 203
DB 24 KLEEMVTVLSDGGIRGIIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 83
QY 204 AMISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGYLMQVLOEKLGETRV 263
DB 84 AMITTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 143
QY 264 HQALTEVAISSFDIKTKNKPVIPTKSNLANSPELDAMKMDICYSTAAAPTYFPFHVTNT 323
DB 144 HQALTEVAISSFDIKTKNKPVIPTKSNLAKSPELDAMKMDICYSTAAAPTYFPFHVTNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALSLISVATRLAQKDPAPASIR 366
DB 204 SNGDIYEFLNVDGAVATVGDPAALSLISVATRLAQEDPAFSSIK 246

RESULT 4

S05592
patatin precursor (clone pPATB2) - potato

C/Species: Solanum tuberosum (potato)

C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C/Accession: S05592

R/Stiekema, W.J.; Heidekamp, F.; Dirkee, W.G.; van Beekun, J.; de Haan, P.; ten Bosch, C

A/Title: Molecular cloning and analysis of four potato tuber mRNAs.

A/Reference number: S05592
A/Accession: S05592
A/Molecule type: mRNA
A/Residues: 1-386 <STI>
A/Cross-references: UNIPROT:P15477; EMBL:X13178; NID:G21509; PIDN:CAA1575.1; PID:G21510
A/Note: the authors translated the codon CAG for residue 288 as Glu and CAA for residue 2
C/Superfamily: patatin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-386/Product: patatin #status predicted <MAT>

Query Match 54.4%; Score 1014; DB 2; Length 386;
Best Local Similarity 88.3%; Pred. No. 7e-66;
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMVTVLSDGGIRGIIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 203
DB 24 KLEEMVTVLSDGGIRGIIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 83
QY 204 AMISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGYLMQVLOEKLGETRV 263
DB 84 AMITTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 143
QY 264 HQALTEVAISSFDIKTKNKPVIPTKSNLANSPELDAMKMDICYSTAAAPTYFPFHVTNT 323
DB 144 HQALTEVAISSFDIKTKNKPVIPTKSNLAKSPELDAMKMDICYSTAAAPTYFPFHVTNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALSLISVATRLAQKDPAPASIR 366
DB 204 SNGARYEFNLVDGAVATVGDPAALSLISVATRLAQEDPAFSSIK 246

RESULT 5

B26017
patatin T58 precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 03-Nov-1987 #sequence_revision 03-Nov-1987 #text_change 09-Jul-2004

C/Accession: B26017

R/Rosahl, S.; Schmidt, R.; Schell, J.; Willmitzer, L.

Mol. Gen. Genet. 203, 214-220, 1986

A/Title: Isolation and characterization of a gene from Solanum tuberosum encoding patatin

A/Reference number: A26017

A/Accession: B26017

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-386 <ROS>

A/Cross-references: UNIPROT:Q41467

C/Superfamily: patatin

Query Match 54.4%; Score 1014; DB 2; Length 386;
Best Local Similarity 88.3%; Pred. No. 7e-66;
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMVTVLSDGGIRGIIIPATILEFLLEGQLQEMDNADARLADYFDVIGSTGGLLT 203
DB 24 KLEEMVTVLSDGGIRGIIIPATILEFLLEGQLQEVNNDKARLADYFDVIGSTGGLLT 83
QY 204 AMISTPENNRPFAAKEIVPFYFEHGPQIFNPSGQILGPKYDGYLMQVLOEKLGETRV 263
DB 84 AMITTPENNRPFAAKDIVPFYFEHGPPIFNYSGSILGPMYDGKYLQVLOEKLGETRV 143
QY 264 HQALTEVAISSFDIKTKNKPVIPTKSNLANSPELDAMKMDICYSTAAAPTYFPFHVTNT 323
DB 144 HQALTEVAISSFDIKTKNKPVIPTKSNLAKSPELDAMKMDICYSTAAAPTYFPFHVTNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALSLISVATRLAQKDPAPASIR 366
DB 204 SNGARYEFNLVDGAVATVGDPAALSLISVATRLAQEDPAFSSIK 246

RESULT 6

A24142
patatin precursor - potato

C/Species: Solanum tuberosum (potato)

C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C/Accession: A24142; S54829
R:Bevan, M.; Barker, R.; Goldbrough, A.; Jarvis, M.; Kavanagh, T.; Iturriaga, G.
Nucleic Acids Res. 14, 4625-4638, 1986
A:Title: The structure and transcription start site of a major potato tuber protein gene
A:Reference number: A24142; PMID:86232596; PMID:3714488
A:Accession: A24142
A:Molecule type: DNA
A:Residues: 1-384 <BEV>
A:Cross-references: UNIPROT:Q9SAP2
R:Zhu, Y.; Dai, W.L.; Liu, J.; Zhao, S.Y.; Wang, X.M.
submitted to the EMBL Data Library, May 1995
A:Description: Isolation and sequence of class I patatin gene from a Chinese potato cult
A:Reference number: S54829
A:Accession: S54829
A:Molecule type: DNA
A:Residues: 1-56, 'p' <ZHU>
A:Cross-references: EMBL:X67216; NID:G809604; PIDN:CAA60675.1; PID:G809605
A:Experimental source: clone 22-1; cultivar Dongnong 303
C:Genetics:
A:Insertions: 56/3; 117/3; 169/3; 224/3; 320/3; 368/3
C:Superfamily: patatin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-384/Product: patatin #status predicted <MAT>

Query Match 54.2%; Score 1011; DB 2; Length 384;
Best Local Similarity 87.8%; Pred. No. 1.1e-65;
Matches 195; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 145 LGEMTVLSTIDGGIGIIPATILEFLEGLOEMDNADARLADYFDVIGSTGGLT 204
DB 25 LGEMTVLSTIDGGIGIIPATILEFLEGLOEDVNNKARLADYFDVIGSTGGLT 84
QY 205 MISTPENNRPPAAKEIVPFYFEGHGPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRV 264
DB 85 MITTPENNRPPAAKDIYVFFYFEGHPIFNYSIGIPRYDGKYLQVLQEKLGSTRV 144
QY 265 QALTEVVISFDIKTKNPVIFTKSNLANSPELDARKYDYSYTAAPTYPPHYFVNTS 324
DB 145 QALTEVAISSFDIKTKNPVIFTKSNLANSPOLDARKYDICYSTAAPIYPPHHFVHTS 204
QY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 205 NGATYEFNLVDGAVATVADPALISVATRLAQEDPAPASSIK 246

RESULT 7
T07592
class I patatin - potato
C/Species: Solanum tuberosum (potato)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C/Accession: T07592
R:Yang, M.S.
submitted to the EMBL Data Library, November 1993
A:Reference number: Z16035
A:Accession: T07592
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-386 <YAN>
A:Cross-references: UNIPROT:Q41487; EMBL:Z27221; NID:G695755; PIDN:CAA81735.1; PID:G6957
A:Experimental source: cv. Sunn; mature plants
A>Note: cDNA, isolated from potato cultivated in Korea
C:Superfamily: patatin

Query Match 53.8%; Score 1004; DB 2; Length 386;
Best Local Similarity 89.2%; Pred. No. 3.7e-65;
Matches 198; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 145 LGEMTVLSTIDGGIGIIPATILEFLEGLOEMDNADARLADYFDVIGSTGGLT 204
DB 25 LGEMTVLSTIDGGIGIIPATILEFLEGLOEDVNNKARLADYFDVIGSTGGLT 84
QY 205 MISTPENNRPPAAKEIVPFYFEGHGPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRV 264

DB 85 MITTPENNRPPAAKEIVPFYFEGHGPQIFNPSGQIFRKYDKYLMQVLQEKLGSTRV 144
QY 265 QALTEVVISFDIKTKNPVIFTKSNLANSPELDARKYDYSYTAAPTYPPHYFVNTS 324
DB 145 QALTEVAISSFDIKTKNPVIFTKSNLANSPOLDARKYDICYSTAAPIYPPHHFVHTS 204
QY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 205 NGATYEFNLVDGAVATVADPALISVATRLAQEDPAPASIR 246

RESULT 8
S05593
patatin precursor (clone pPATn) - potato (fragment)
N/Contains: proteinase inhibitor II
C/Species: Solanum tuberosum (potato)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C/Accession: S05593
R:Stiekema, W.J.; Heidekamp, F.; Dirkse, W.G.; van Beckum, J.; de Haan, P.; ten Bosch, C.
Plant Mol. Biol. 11, 255-269, 1988
A:Title: Molecular cloning and analysis of four potato tuber mRNAs.
A:Reference number: S05592
A:Accession: S05593
A:Molecule type: mRNA
A:Residues: 1-377 <STI>
A:Cross-references: UNIPROT:P15476; EMBL:X13179; NID:G21507; PIDN:CAA31576.1; PID:G80506;
A>Note: the authors translated the codon CAG for residue 288 as Glu and CAA for residue 2
F:15-377/Product: patatin #status predicted <MAT>

Query Match 53.7%; Score 1002; DB 2; Length 377;
Best Local Similarity 87.0%; Pred. No. 5e-65;
Matches 194; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 144 QLGEMTVLSTIDGGIGIIPATILEFLEGLOEMDNADARLADYFDVIGSTGGLT 203
DB 15 KLEEMTVLSTIDGGIGIIPATILEFLEGLOEDVNNKARLADYFDVIGSTGGLT 74
QY 204 AMISTPENNRPPAAKEIVPFYFEGHGPQIFNPSGQILGPKYDKYLMQVLQEKLGSTRV 263
DB 75 AMITTPENNRPPAAANDIYVFFYFEGHPIFNYSIGIPRYDGKYLQVLQEKLGSTRV 134
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDARKYDYSYTAAPTYPPHYFVNTS 323
DB 135 HQALTEVAISSFDIKTKNPVIFTKSNLANSPELDARKYDICYSTAAPIYPPHHFVHTS 194
QY 324 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 195 NGATYEFNLVDGAVATVADPALISVATRLAQEDPAPASSIK 237

RESULT 9
T03841
patatin homolog - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T03841
R:Drews, G.N.; Beale, T.P.; Bul, A.Q.; Goldberg, R.B.
Plant Cell 4, 1383-1404, 1992
A:Title: Regional and cell-specific gene expression patterns during petal development.
A:Reference number: Z15112; PMID:9310883; PMID:1477354
A:Accession: T03841
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-390 <DBE>
A:Cross-references: UNIPROT:O24152; EMBL:U68484; NID:G1546816; PIDN:AA808428.1; PID:G1546
C:Superfamily: patatin

Query Match 41.7%; Score 778.5; DB 2; Length 390;
Best Local Similarity 67.1%; Pred. No. 8.1e-49;
Matches 151; Conservative 31; Mismatches 36; Indels 7; Gaps 4;

T00989
N: hypothetical protein At2g26560 [imported] - Arabidopsis thaliana
N: Alternate names: patatin homolog T9J22.23
C: Species: Arabidopsis thaliana (mouse-ear cress)
C: Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C: Accession: T00989; A84662
R: Rounsley, S.D.; Lin, X.; Kelchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, April 1998
A: Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.
A: Reference number: Z14161
A: Accession: T00989
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-407 <ROU>
A: Cross-references: UNIPROT:O48723; EMBL:AC002505; NID:g2739359; PIDN:AAC14504.1; PID:g2739359
A: Experimental source: cultivar Columbia
R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.B.; Unayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, D.
Nature 402, 761-768, 1999
A: Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A: Reference number: A84420; MUID:20083487; PMID:10617197
A: Accession: A84662
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-407 <STO>
A: Cross-references: GB:AE002093; NID:g2739381; PIDN:AAC14504.1; GSPDB:GN00139
C: Genetics:
A: Gene: At2g26560; T9J22.23
A: Map position: 2
A: Introns: 46/3; 169/3; 223/3; 324/3; 382/2
C: Superfamily: patatin

Query Match 30.5%; Score 569.5; DB 2; Length 407;
Best Local Similarity 51.8%; Pred. No. 1.2e-33;
Matches 116; Conservative 32; Mismatches 65; Indels 13; Gaps 3;

QY 137 KASYGPGQLGEMVTVLSIDGGGIRGIIPATLLEFLGQLQGMNNADARLADYFDVIGT 196
Db 7 KSPLOPPYGNLVITLSDGGGIRGLIPAVILGFLESLQQLDGB-EARLADYFDVIAGT 65

QY 197 STGGLTMTMTPEHNNRPFPAAKEIVPFYFEHGRQIFNPS-----GGILPRKY 245
Db 66 STGGIVTAMTLPAAPKKEGRPLFAASEIKDFYLEQCEPKIPDHPFPPSAKKLVKSLTGPKY 125

QY 246 DGKIMQVLQEKLETRVHQALTEVVISPDITKNKPVYFTRKSLANSPELDAMVYDISY 305
Db 126 DGKILHQLIAKKLGGDTKLSQTLTNVVIPTPIKHLQPTTSSYEYKHNPLKDAITLADIAT 185

QY 306 STAAATPFPFPFHYEVTWTSNGDEYEFNLVDGAVA TVADPALLSISVAT 353
Db 186 STSAPATPLPAHFFKVEDLNGNAKEYNLIDGVA-ANNPALLAIGEVY 232

RESULT 14
F85437
patatin-like protein [imported] - Arabidopsis thaliana
C: Species: Arabidopsis thaliana (mouse-ear cress)
C: Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C: Accession: F85437
R: anonymous; The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Harbor Laboratory, 1999
A: Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A: Reference number: A85001; MUID:20083488; PMID:10617198
A: Accession: F85437
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-428 <STO>
C: Genetics:
A: Gene: AT4g37050
A: Map position: 4
C: Superfamily: patatin

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Query Match          30.0%; Score 560; DB 2; Length 428;
Best Local Similarity 48.0%; Pred. No. 6.3e-33;
Matches 117; Conservative 43; Mismatches 62; Indels 22; Gaps 6;

QY      142 PGQLGEMTVLSDGGIRGIIPATILFLEQLOEMDNADRLADYPDVGISTGTGL 201
Db       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy       28 PPSVGLATLTISIDGGIRGIIPGITLLAVLESQLOELDDB-EARLVDPVISIGTSTGL 86
QY      202 LTAIVISTPNE-----NRRPAAAKEIYFPFEHGPOLF-NPSG-----QILG 242
Db       |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy       87 IVAMLTLDODSGHSRNSNRPLFEAKKEIYFPFLKHSPKIFPPORGIFFCGNETIVRVGG 146
QY      243 PKYQGKYLMOVLQEDGETRVHQALTEVVISSEFDIKTNKPVIPTKSNLANSPELDARMYD 302
Db       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy      147 PKENGKYLHDVEGFLGDTKLQTSLTNVVI PCFDIKLPVFSSIQAVNNQANNAKTLSD 206
QY      303 ISYSTAAPTYFPFPHYFVTNTSNGDEYEENLVDAVATVADPALLSISVATR-LAOKDPA 361
Db       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy     207 ICISTSAAPTFPPAHRFINDESEGFKHEFNLLDGIIA-ANNPFLCALIAETVKQIIKKNPV 265
QY      362 FASIT 365
Db       266 MGDI 269

RESULT 15
TI0260 pataatin-like protein - cucumer (fragment)
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 09-Jul-2004
C:Accession: TI0260
R:Praisig-Mueller, R.; May, C.; Hoehne, M.; Gnan, P.; Kindl, H.
Submitted to the EMBL Data Library, April 1997
A:Description: Is the pataatin-like protein localized to lipid bodies involved in the mobi
A:Reference number: Z17002
A:Accession: TI0260
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-405 <PRE>
A:Cross-references: UNIPROT:O23784; EMBL:Y12793
A:Experimental source: cotyledon
C:Function:
A:Description: mobilization of fat during seed germination
C:Superfamily: pataatin

Query Match          27.2%; Score 507.5; DB 2; Length 405;
Best Local Similarity 46.8%; Pred. No. 3.7e-29;
Matches 103; Conservative 44; Mismatches 60; Indels 13; Gaps 3;

QY      146 GEMTVLSDGGIRGIIPATILFLEQLOEMDNADRLADYPVIGSTSGGLTTAM 205
Db       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy      21 GKMTLTISIDGGIRGIIPSTILLAFLESKLQELD-GPDVRIDYFVIAIGTSGGLVTSM 79
QY      206 ISTEENNRRPFAAKEIYFPFEHGPOLF-----NPSGQILGPXYDKYLMQVL 254
Db       ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy      80 LTADPDKNRRPLYSASDLALFYIEHAKPIFPQNRYFLCSLVNPFPGXVMGPRYNGLYRSLL 139
QY      255 QEKLGTRVHQALTEVVISSEFDIKTNKPVIPTKSNLANSPELDARMYDISYSTAAPTYF 314
Db       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy     140 KGLAGDITLKQTLSSQVVIPAFDIKLPVIFTTIAKCELNKPNKLADVCISTSAAPTFL 199
QY      315 PPHYFVTNTSNGDEYEENLVDAVATVADPALLSISVATR 354
Db       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dy     200 PGEYEQTKDSKGNIRNYEMVDGVA-ANNPFLAAMTHVTK 238

Search completed: April 8, 2005, 07:57:03
Job time : 46 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 07:26:08 ; Search time 182 Seconds
(without alignments)
1029.786 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNKKMALLSLGTGTTSEF.....LSISVATRLAQKDPAFASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1139 | 61.1 | 386 | 2 | Q8LPW4 solanum car |
| 2 | 1033 | 55.4 | 386 | 1 | PAT5 SOLTU |
| 3 | 1033 | 55.4 | 386 | 2 | Q42502 solanum tub |
| 4 | 1033 | 55.4 | 386 | 2 | Q42502 solanum tub |
| 5 | 1017 | 54.5 | 386 | 1 | Q7DMP8 solanum bre |
| 6 | 1014 | 54.4 | 386 | 1 | PAT0 SOLTU |
| 7 | 1014 | 54.4 | 386 | 1 | PAT2 SOLTU |
| 8 | 1004 | 53.8 | 386 | 2 | Q41467 solanum tub |
| 9 | 1002 | 53.7 | 377 | 1 | PAT1 SOLTU |
| 10 | 1002 | 53.7 | 386 | 2 | Q41467 solanum tub |
| 11 | 996.5 | 53.4 | 387 | 2 | Q8LSC1 solanum cha |
| 12 | 778.5 | 41.7 | 263 | 2 | Q7DMC7 solanum cha |
| 13 | 778.5 | 41.7 | 390 | 2 | Q24152 nicotiana t |
| 14 | 614 | 32.9 | 383 | 2 | Q8LBT5 arabiidopsis |
| 15 | 614 | 32.9 | 414 | 2 | Q23179 arabiidopsis |
| 16 | 613 | 32.9 | 420 | 2 | Q9FZ09 nicotiana t |
| 17 | 612 | 32.8 | 410 | 2 | Q23148 arabiidopsis |
| 18 | 609.5 | 32.7 | 405 | 2 | Q6ZUD3 oryza sativ |
| 19 | 585 | 31.4 | 387 | 2 | Q67121 oryza sativ |
| 20 | 579 | 31.0 | 400 | 2 | Q9AQ78 hevea bras |
| 21 | 575 | 30.8 | 414 | 2 | Q23180 arabiidopsis |
| 22 | 569.5 | 30.5 | 405 | 2 | Q8LDB8 arabiidopsis |
| 23 | 569.5 | 30.5 | 407 | 2 | Q48723 arabiidopsis |
| 24 | 560 | 30.0 | 428 | 2 | Q23181 arabiidopsis |
| 25 | 545 | 29.2 | 442 | 2 | Q8GVV8 oryza sativ |
| 26 | 544.5 | 29.2 | 431 | 2 | Q6ZG42 oryza sativ |
| 27 | 543 | 29.1 | 411 | 2 | Q9FZ08 nicotiana t |
| 28 | 537.5 | 28.8 | 430 | 2 | Q6ZG46 oryza sativ |
| 29 | 529.5 | 28.4 | 207 | 2 | Q9FZ07 nicotiana t |
| 30 | 527 | 28.3 | 401 | 2 | Q9F1Y1 arabiidopsis |
| 31 | 525.5 | 28.2 | 410 | 2 | Q9XE75 sorghum bic |

| | | | | | |
|----|-------|------|-----|---|---------------------|
| 32 | 515 | 27.6 | 422 | 2 | Q9XE77 sorghum bic |
| 33 | 511 | 27.4 | 411 | 2 | Q8S0B1 oryza sativ |
| 34 | 507.5 | 27.2 | 405 | 2 | Q23784 cucumis sat |
| 35 | 494.5 | 26.5 | 432 | 2 | Q840Y3 oryza sativ |
| 36 | 491.5 | 26.4 | 438 | 2 | Q9XE79 sorghum bic |
| 37 | 462.5 | 24.8 | 388 | 2 | Q81984 hevea bras |
| 38 | 458.5 | 24.6 | 387 | 2 | Q706V4 hevea bras |
| 39 | 458.5 | 24.6 | 388 | 2 | Q9SEM0 hevea bras |
| 40 | 454.5 | 24.4 | 388 | 2 | Q65811 hevea bras |
| 41 | 450.5 | 24.2 | 388 | 2 | Q04008 hevea bras |
| 42 | 341.5 | 18.3 | 339 | 2 | Q8L3P2 arabiidopsis |
| 43 | 288.5 | 15.5 | 302 | 2 | Q8YUN7 arabidopsis |
| 44 | 287 | 15.4 | 302 | 2 | Q73HJ4 wolbachia p |
| 45 | 284.5 | 15.3 | 499 | 2 | Q80959 arabiidopsis |

ALIGNMENTS

RESULT 1

| ID | Q8LPW4 | PRELIMINARY; | PRT; | 386 AA. |
|----|--|--------------|------|---------|
| AC | Q8LPW4; | | | |
| DT | 01-OCT-2002 (TREMREL. 22, Created) | | | |
| DT | 01-OCT-2002 (TREMREL. 22, Last sequence update) | | | |
| DT | 01-MAR-2004 (TREMREL. 26, Last annotation update) | | | |
| DE | Patacin. | | | |
| OS | Solanum cardiophyllum. | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; | | | |
| OC | lamiales; Solanales; Solanaceae; Solanum. | | | |
| OX | NCBI_TaxID=160510; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=22664533; PubMed=12779324; DOI=10.1021/bi027156r; | | | |
| RA | Rydell T.J., Williams J.M., Krieger E., Moshiri F., Stallings W.C., | | | |
| RA | Brown S.M., Pershing J.C., Purcell J.P., Alibhai M.F.; | | | |
| RT | "The crystal structure, mutagenesis, and activity studies reveal that | | | |
| RT | patacin is a lipid acyl hydrolase with a Ser-Asp catalytic dyad." | | | |
| RL | Biochemistry 42:6696-6708(2003). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Joyce E.K., Levine B., Isaac B., Brown S.M., Pershing J.C., | | | |
| RA | Purcell J.P., Alibhai M.F.; | | | |
| RL | Submitted (APR-2001) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AY033231; AAK5395.1; - | | | |
| DR | PDB; 1OXW; X-ray; A/B/C=14-386. | | | |
| DR | GO; GO:0003824; F:catalytic activity; IEA. | | | |
| DR | GO; GO:0045735; F:nutrient reservoir activity; IEA. | | | |
| DR | InterPro; IPR002641; Patacin. | | | |
| DR | Pfam; PF01734; Patacin.1. | | | |
| SO | SEQUENCE 386 AA; 42486 MW; 30C56BA86A024282 CRC64; | | | |

Query Match 61.1%; Score 1139; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.9e-69;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 144 | QLGEMVTLSIDGGGIRGIIPATILFEFLGQLOEMDNADRLADYDVIGTSGILLT | 203 |
| DB | 24 | QLGEMVTLSIDGGGIRGIIPATILFEFLGQLOEMDNADRLADYDVIGTSGILLT | 83 |
| QY | 204 | AMSTPENNRPFAAAKEIYPFPEHGPOIFNPSGQILGKYGKTYMOVLQELGSTRV | 263 |
| DB | 84 | AMSTPENNRPFAAAKEIYPFPEHGPOIFNPSGQILGKYGKTYMOVLQELGSTRV | 143 |
| QY | 264 | HQALTEVVISFDIKTKNPVIFTKSNLANSPELDAXKYDISYTAAPTFPPHYFTVNT | 323 |
| DB | 144 | HQALTEVVISFDIKTKNPVIFTKSNLANSPELDAXKYDISYTAAPTFPPHYFTVNT | 203 |
| QY | 324 | SNDEYEFNVDGAVATVADPALISVATRLAQKDPAFASIR | 366 |
| DB | 204 | SNDEYEFNVDGAVATVADPALISVATRLAQKDPAFASIR | 246 |

```

RESULT 2
PATS_SOLTU STANDARD; PRT; 386 AA.
ID PATS_SOLTU STANDARD; PRT; 386 AA.
AC P15478;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Patatin T5 precursor (Potato tuber protein).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Rosahl S., Schmidt R., Schell J., Willmitzer L.;
RT "Isolation and characterization of a gene from Solanum tuberosum
RT encoding patatin, the major storage protein of potato tubers."
RL Mol. Genet. 203:214-220(1986).
CC -1- FUNCTION: Patatin may have a dual role as a somatic storage
CC protein and as an enzyme involved in host resistance. This tuber
CC protein represents approximately 40% of the total protein in
CC mature tubers.
CC -1- MISCELLANEOUS: There is strong evidence that patatin is a
CC lipolytic acyl hydrolase (LAH), an activity which is thought to be
CC involved in the response of tubers to pathogens.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; X03932; CA27571.1; -
DR PIR; A26017; A26017.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
KM Glycoprotein; Hydrolase; Multigene family; Signal; Storage protein.
FT CHAIN 1 23
FT SIGNAL 1 23
FT CARBOHYD 24 386
FT CARBOHYD 60 60
FT CARBOHYD 90 90
FT CARBOHYD 202 202
SQ SEQUENCE 386 AA; 42338 MW; E7F7PAD1A04A1000 CRC64;

Query Match 55.4%; Score 1033; DB 1; Length 386;
Best Local Similarity 90.1%; Pred. No. 7.5e-62;
Matches 200; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 145 LGEWVTVLSIDGGIRGIIIPATILEPFLGQLOEMDNADRLADYPIVIGSTGGLTA 204
DB 25 LGEWVTVLSIDGGIRGIIIPATILEPFLGQLOEMDNADRLADYPIVIGSTGGLTA 84
OY 205 MISTPENNRRPFAAKEIVPFYFEGHPQIFNPSGQILGPKYDKYLMQVLOEKLGETRVH 264
DB 85 MISTPENNRRPFAAKEIVPFYFEGHPQIFNPSGQILGPKYDKYLMQVLOEKLGETRVH 144
OY 265 QALTEVVISFDIKTKKPYVFTKSNLANSPELDKMYDISYTRAAFTYPPHYFTVNTS 324
DB 145 QALTEVVISFDIKTKKPYVFTKSNLANSPELDKMYDISYTRAAFTYPPHYFTVNTS 204
OY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAFASIR 366
DB 205 NGDKTEFNLVDGAVATVADPALISVATRLAQKDPAFASIR 246

RESULT 3
O42502 PRELIMINARY; PRT; 386 AA.
AC O42502;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Patatin precursor.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062793; PubMed=6150463;
RA Mignery G.A., Pikaard C.S., Hannapel D.J., Park W.D.;
RT "Isolation and sequence analysis of cDNAs for the major potato tuber
RT protein, patatin."
RL Nucleic Acids Res. 12:7987-8000(1984).
DR EMBL; X01125; CA25592.1; -
DR PIR; S51596; S51596.
DR HSP; Q8LPW4; 10XW.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
KM Signal.
FT CHAIN 1 23
FT SIGNAL 1 23
FT CHAIN 24 386
SQ SEQUENCE 386 AA; 42465 MW; 178107C161B7DEBD CRC64;

Query Match 55.4%; Score 1033; DB 2; Length 386;
Best Local Similarity 89.6%; Pred. No. 7.5e-62;
Matches 199; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

OY 145 LGEWVTVLSIDGGIRGIIIPATILEPFLGQLOEMDNADRLADYPIVIGSTGGLTA 204
DB 25 LGEWVTVLSIDGGIRGIIIPATILEPFLGQLOEMDNADRLADYPIVIGSTGGLTA 84
OY 205 MISTPENNRRPFAAKEIVPFYFEGHPQIFNPSGQILGPKYDKYLMQVLOEKLGETRVH 264
DB 85 MISTPENNRRPFAAKEIVPFYFEGHPQIFNPSGQILGPKYDKYLMQVLOEKLGETRVH 144
OY 265 QALTEVVISFDIKTKKPYVFTKSNLANSPELDKMYDISYTRAAFTYPPHYFTVNTS 324
DB 145 QALTEVVISFDIKTKKPYVFTKSNLANSPELDKMYDISYTRAAFTYPPHYFTVNTS 204
OY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAFASIR 366
DB 205 NGDKTEFNLVDGAVATVADPALISVATRLAQKDPAFASIR 246

RESULT 4
O7DMP8 PRELIMINARY; PRT; 386 AA.
ID O7DMP8 PRELIMINARY; PRT; 386 AA.
AC O7DMP8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Patatin precursor.
OS Solanum brevifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4115;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95107249; PubMed=7808402;
RA Banfalvi Z., Kostyal Z., Barta E.;
RT "Solanum brevifolius possesses a non-sucrose-inducible patatin gene."
RL Mol. Genet. 245:517-522(1994).
DR EMBL; U09331; AA66198.1; -
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.

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KW Signal.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 386 Patatin.
 SQ SEQUENCE 386 AA; 42465 MW; 178107C61B7DEB CRC64;

Query Match 55.4%; Score 1033; DB 2; Length 386;
 Best Local Similarity 89.6%; Pred. No. 7.5e-62;
 Matches 199; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 145 LGEMVTVLSIDGGIGIIPATILEPFLBEGLOEMDNADRLADYFDVIGTSGGLTTA 204
 |||
 DB 25 LGEMVTVLSIDGGIGIIPATILEPFLBEGLOEMDNADRLADYFDVIGTSGGLTTA 84
 |||

QY 205 MISTPENNRRPPAAKEIVPEFEEHGPQIFNPSGQILGPKYDGKYLMOVLQOEKLGSTRV 264
 |||
 DB 85 MISTPENNRRPPAAKDIIVPEFEEHGPHTNNSGSGIPMYDGKIFLOVLQOEKLGSTRV 144
 |||

QY 265 QALTEVVISFPIKTKNPVIFTKSNLANSPELDAAKMYDISYSTAAAPTYPPHYFTNTS 324
 |||
 DB 145 QALTEVAISSFDIKTKNPVIFTKSNLANSPELDAAKMYDICYSTAAAPTYPPHYFTHTS 204
 |||

QY 325 NGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
 |||
 DB 205 NGDKYEFNLVDGAVATVADPALLSLSVATRLAQVDPAPASIK 246
 |||

RESULT 5
 PAT3_SOLTU STANDARD; PRT; 386 AA.
 ID PAT3_SOLTU
 AC P11768;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Patatin class I precursor (Potato tuber protein).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteride;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 NC NCBITaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Superior;
 RX MEDLINE=88226014; PubMed=37371664; DOI=10.1016/0378-1119(88)90577-X;
 RA Mignery G.A., Pikaard C.S., Park M.D.;
 RT "Molecular characterization of the patatin multigene family of
 potato.";
 RL Gene 62:27-44(1988).
 CC -1- FUNCTION: Patatin may have a dual role as a somatic storage
 protein and as an enzyme involved in host resistance. This tuber
 protein represents approximately 40% of the total protein in
 mature tubers.
 CC -1- MISCELLANEOUS: There is strong evidence that patatin is a
 lipolytic acyl hydrolase (LAH), an activity which is thought to be
 involved in the response of tubers to pathogens.
 CC -----
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 CC -----
 CC EMBL; M18880; AAA33819.1; -;
 DR EMBL; M18883; AAA33831.1; -;
 DR PIR; A29810; A29810.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF01734; Patatin; 1.
 KW Glycoprotein; Hydrolase; Multigene family; Signal; Storage protein.
 FT SIGNAL 1 23
 FT CHAIN 24 386 Patatin class I.
 FT CARBOHYD 115 115 N-linked (GLCNAC...) (Potential).
 SQ SEQUENCE 386 AA; 42651 MW; 7A20AFAAACD85229 CRC64;

Query Match 54.5%; Score 1017; DB 1; Length 386;
 Best Local Similarity 87.9%; Pred. No. 9.1e-61;
 Matches 196; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLGEMVTVLSIDGGIGIIPATILEPFLBEGLOEMDNADRLADYFDVIGTSGGLTT 203
 |||
 DB 24 KLEEMVTVLSIDGGIGIIPATILEPFLBEGLOEMDNADRLADYFDVIGTSGGLTT 83
 |||

QY 204 AMISTENNRRPPAAKEIVPEFEEHGPQIFNPSGQILGPKYDGKYLMOVLQOEKLGSTRV 263
 |||
 DB 84 AMISTENNRRPPAAKDIIVPEFEEHGPHTNNSGSGIPMYDGKIFLOVLQOEKLGSTRV 143
 |||

QY 264 HQALTEVVISFPIKTKNPVIFTKSNLANSPELDAAKMYDISYSTAAAPTYPPHYFTNTS 323
 |||
 DB 144 HQALTEVAISSFDIKTKNPVIFTKSNLANSPELDAAKMYDICYSTAAAPTYPPHYFTHT 203
 |||

QY 324 SNDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
 |||
 DB 204 SNQDIYEFNLVDGAVATVADPALLSLSVATRLAQEDPAPASIK 246
 |||

RESULT 6
 PAT3_SOLTU STANDARD; PRT; 386 AA.
 ID PAT3_SOLTU
 AC P07745;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Patatin precursor (Potato tuber protein).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteride;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 NC NCBITaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Maris Piper 6094;
 RX MEDLINE=86232596; PubMed=37144488;
 RA Bevan M., Barker R., Goldsbrough A., Jarvis M., Kavanagh T.,
 RA Icuriaga G.;
 RT "The structure and transcription start site of a major potato tuber
 RT protein gene.";
 RL Nucleic Acids Res. 14:4625-4638(1986).
 CC -1- FUNCTION: Patatin may have a dual role as a somatic storage
 protein and as an enzyme involved in host resistance. This tuber
 CC protein represents approximately 40% of the total protein in
 CC mature tubers.
 CC -1- MISCELLANEOUS: There is strong evidence that patatin is a
 CC lipolytic acyl hydrolase (LAH), an activity which is thought to be
 CC involved in the response of tubers to pathogens.
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 CC -----
 CC EMBL; X03956; CAA27588.1; -;
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF01734; Patatin; 1.
 KW Glycoprotein; Hydrolase; Multigene family; Signal; Storage protein.
 FT SIGNAL 1 23
 FT CHAIN 24 386 Patatin.
 FT CARBOHYD 115 115 N-linked (GLCNAC...) (Potential).
 SQ SEQUENCE 386 AA; 42490 MW; CF455970CCDB10B7 CRC64;

Query Match 54.4%; Score 1014; DB 1; Length 386;
 Best Local Similarity 88.3%; Pred. No. 1.5e-60;
 Matches 196; Conservative 12; Mismatches 14; Indels 0; Gaps 0;


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QY 145 LGMVTVLSIDGGIGRIIPATILEFLBEGLOEMDNADARLADYDVIGSTGGLT 204
DB 25 LGMVTVLSIDGGIGRIIPATILEFLBEGLOEMDNADARLADYDVIGSTGGLT 84
QY 205 MISTPENNRPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 264
DB 85 MISTPENNRPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 144
QY 265 QALTEVVISFPIKTKKPVIFTKSNLANSPELDKMYDISYTAAPTYPPHYFVNTS 324
DB 145 QALTEVVISFPIKTKKPVIFTKSNLANSPELDKMYDISYTAAPTYPPHYFVNTS 204

QY 325 NGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 366
DB 205 NGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 246

RESULT 7
PAT2_SOLUTU STANDARD; PRT; 386 AA.
ID PAT2_SOLUTU STANDARD; PRT; 386 AA.
AC P15477;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Patatin B2 precursor (Potato tuber protein).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Bintje;
RA Stiekema W.J., Heidekamp F., Dirkse W.G., van Beckum J., de Haan P.,
RA ten Bosch C., Louwerse J.D.;
RT "Molecular cloning and analysis of four potato tuber mRNAs.";
RT Plant Mol. Biol. 11:255-269(1988).
CC -1- FUNCTION: Patatin may have a dual role as a somatic storage
CC protein and as an enzyme involved in host resistance. This tuber
CC protein represents approximately 40% of the total protein in
CC mature tubers.
CC -1- MISCELLANEOUS: There is strong evidence that patatin is a
CC lipolytic acyl hydrolase (LH), an activity which is thought to be
CC involved in the response of tubers to pathogens.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X13178; CAJ31575.1; -.
DR PIR, S05592; S05592.
DR InterPro, IPR002641; Patatin.
DR Pfam, PF01734; Patatin; 1.
KW Glycoprotein; Hydrolase; Multigene family; Signal; Storage protein.
FT CHAIN 1 23
FT SIGNAL 1 23
FT CARBOHYD 24 386 Patatin B2.
FT CARBOHYD 115 115 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 325 325 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 386 AA; 42612 MW; 5C0518B6A282405 CRC64;

Query Match 54.4%; Score 1014; DB 1; Length 386;
Best Local Similarity 88.3%; Pred. No. 1.5e-60;
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
QY 144 QLGEMTVLSIDGGIGRIIPATILEFLBEGLOEMDNADARLADYDVIGSTGGLT 203
DB 24 KLEEMTVLSIDGGIGRIIPATILEFLBEGLOEMDNADARLADYDVIGSTGGLT 83
QY 204 AMISTPENNRPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 263

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DB 84 AMISTPENNRPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 143
QY 264 HQALTEVVISFPIKTKKPVIFTKSNLANSPELDKMYDISYTAAPTYPPHYFVNT 323
DB 144 HQALTEVVISFPIKTKKPVIFTKSNLANSPELDKMYDISYTAAPTYPPHYFVNT 203
QY 324 SNGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 366
DB 204 SNGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 246

RESULT 8
Q41487 PRELIMINARY; PRT; 386 AA.
ID Q41487 PRELIMINARY; PRT; 386 AA.
AC Q41487; Q41473;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Patatin.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang M.J., Yang M.S.;
RT "Nucleotide Sequences of Class I Patatin cDNA from Potato Cultivated
RT in Korea.";
RT Plant Mol. Biol. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang M.S.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL, Z27221; CA81735.1; -.
DR PIR, A23634; A23634.
DR PIR, T07592; T07592.
DR HSSP, Q8LPM4; 10XW.
DR GO, GO:0003824; F:catalytic activity; IEA.
DR GO, GO:0045735; F:nucleic acid reservoir activity; IEA.
DR InterPro, IPR002641; Patatin.
DR Pfam, PF01734; Patatin; 1.
SQ SEQUENCE 386 AA; 42628 MW; A58E1DC9529B0DF CRC64;

Query Match 53.8%; Score 1004; DB 2; Length 386;
Best Local Similarity 89.2%; Pred. No. 7e-60;
Matches 198; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
QY 145 LGMVTVLSIDGGIGRIIPATILEFLBEGLOEMDNADARLADYDVIGSTGGLT 204
DB 25 LGMVTVLSIDGGIGRIIPATILEFLBEGLOEMDNADARLADYDVIGSTGGLT 84
QY 205 MISTPENNRPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 264
DB 85 MISTPENNRPAAAKEIVPFYFHEGPHIFNSGQILGPKYDKYLMQVLOEKLGETRV 144
QY 265 QALTEVVISFPIKTKKPVIFTKSNLANSPELDKMYDISYTAAPTYPPHYFVNTS 324
DB 145 QALTEVVISFPIKTKKPVIFTKSNLANSPELDKMYDISYTAAPTYPPHYFVNTS 204
QY 325 NGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 366
DB 205 NGDEYFNLVDGAVATVADPALLISVATRLAQKDPAPASIR 246

RESULT 9
PAT1_SOLUTU STANDARD; PRT; 377 AA.
ID PAT1_SOLUTU STANDARD; PRT; 377 AA.
AC P15476;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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Db      24 KLEEMTVLSTIDGGIGIIPATILEFEQLOEMDNNAARLADYFDVIGSTGILLT 83
Qy      204 AMISTENNRRPFAAKEIIVPFYFEGHGPQIFNPSG--ILGPKYDGKYLMOVLQEKLGETR 262
Db      84 AMITTENNRRPFAAKDIPFYPFEGHGPQIFNPSGRIFPMTDGNLLOVLQEKLGETR 143
Qy      263 VHQALTEVVISFDIKTKKPVIFTKSNLANSPEIDAKMYDISYSTAAAPTYPPHYFVTN 322
Db      144 VHQALTEVVISFDIKTKKPVIFTKSNLAKSPEDAKMYDICYSTAAAPTYPPHYFVTN 203
Qy      323 TNSGDEYEFNLVDGAVATVADPALISVATRLAQCDPAFASIR 366
Db      204 TNSGDIYEFNLVDGAVATVADPALISVATRLAQEDPAFASIR 247

RESULT 12
ID      07DMC7      PRELIMINARY;      PRT;      263 AA.
AC      07DMC7;
DT      05-JUL-2004 (T-EMBLrel. 27, Created)
DT      05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE      05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DR      Patatin homolog (Fragment).
OS      Nicotiana glauca (Common tobacco).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      Lamiales; Solanales; Solanaceae; Nicotiana.
OX      NCBI_TaxID=4097;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93120883; PubMed=1477554;
RA      Drews G.N., Beals T.P., Bui A.Q., Goldberg R.B.;
RT      "Regional and cell-specific gene expression patterns during petal
RT      development.";
RL      Plant Cell 4:1383-1404(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      Beals T.P., Goldberg R.B.;
RA      Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RL      EMBL; U68483; AAB08427.1; -.
DR      GO; GO:0003824; F:catalytic activity; IEA.
DR      GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR      InterPro; IPR002641; Patatin.
DR      Pfam; PF01734; Patatin; 1.
FT      NON TER      263
SQ      SEQUENCE 263 AA; 28225 MW; 66D617A7F0C7FBF3 CRC64;

Query Match      41.7%; Score 778.5; DB 2; Length 263;
Best Local Similarity 67.1%; Pred. No. 8e-45;
Matches 151; Conservative 31; Mismatches 36; Indels 7; Gaps 4;

Qy      145 LGEWTVLSTIDGGIGIIPATILEFEQLOEMDNNAARLADYFDVIGSTGILLT 204
Db      25 VGSIAVTLSTIDGGIGIIPATVLSFESQLQEDNNEDARLADYFDVIGSTGILLT 84
Qy      205 MISTENNRRPFAAKEIIVPFYFEGHGPQIFNPSG--QILGPKYDGKYLMOVLQEKLGETR 261
Db      85 MISAPNEKRPFAAKDIVSFYFEGHGPQIFNPSG--PGVWPPIIGPKYDGKYLMOVLQEKLGETR 143
Qy      262 RVHQALTEVVISFDIKTKKPVIFTKSNLANSPEIDAKMYDISYSTAAAPTYPPHYFVTN 321
Db      144 RVHQALTEVVISFDIKTKKPVIFTKSEIANSPEIDAKMYDICYSTAAAPTYPPHYFVTN 203
Qy      322 NTNSGDEYEFNLVDGAVATVADPALISVATRLAQCDPAFASIR 366
Db      204 DDKGNQHEFNLDGGVAV--NPALIAVSTYTK--SVDPVSASIK 245

RESULT 13
ID      024152      PRELIMINARY;      PRT;      390 AA.
AC      024152;

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DT      01-JAN-1998 (T-EMBLrel. 05, Created)
DT      01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT      01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE      Patatin homolog.
OS      Nicotiana glauca (Common tobacco).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      Lamiales; Solanales; Solanaceae; Nicotiana.
OX      NCBI_TaxID=4097;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93120883; PubMed=1477554;
RA      Drews G.N., Beals T.P., Bui A.Q., Goldberg R.B.;
RT      "Regional and cell-specific gene expression patterns during petal
RT      development.";
RL      Plant Cell 4:1383-1404(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      Beals Thomas P., Goldberg R.B.;
RL      Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U68484; AAB08428.1; -.
DR      PIR; T03841; T03841.
DR      HSSP; O8LPM4; 10XM.
DR      GO; GO:0003824; F:catalytic activity; IEA.
DR      GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR      InterPro; IPR002641; Patatin.
DR      Pfam; PF01734; Patatin; 1.
SQ      SEQUENCE 390 AA; 42499 MW; 9A70F5D9C85DB5F CRC64;

Query Match      41.7%; Score 778.5; DB 2; Length 390;
Best Local Similarity 67.1%; Pred. No. 1.4e-44;
Matches 151; Conservative 31; Mismatches 36; Indels 7; Gaps 4;

Qy      145 LGEWTVLSTIDGGIGIIPATILEFEQLOEMDNNAARLADYFDVIGSTGILLT 204
Db      25 VGSIAVTLSTIDGGIGIIPATVLSFESQLQEDNNEDARLADYFDVIGSTGILLT 84
Qy      205 MISTENNRRPFAAKEIIVPFYFEGHGPQIFNPSG--QILGPKYDGKYLMOVLQEKLGETR 261
Db      85 MISAPNEKRPFAAKDIVSFYFEGHGPQIFNPSG--PGVWPPIIGPKYDGKYLMOVLQEKLGETR 143
Qy      262 RVHQALTEVVISFDIKTKKPVIFTKSNLANSPEIDAKMYDISYSTAAAPTYPPHYFVTN 321
Db      144 RVHQALTEVVISFDIKTKKPVIFTKSEIANSPEIDAKMYDICYSTAAAPTYPPHYFVTN 203
Qy      322 NTNSGDEYEFNLVDGAVATVADPALISVATRLAQCDPAFASIR 366
Db      204 DDKGNQHEFNLDGGVAV--NPALIAVSTYTK--SVDPVSASIK 245

RESULT 14
ID      08LBT5      PRELIMINARY;      PRT;      383 AA.
AC      08LBT5;
DT      01-OCT-2002 (T-EMBLrel. 22, Created)
DT      01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE      01-OCT-2002 (T-EMBLrel. 25, Last annotation update)
DR      Patatin-like protein.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22088475; PubMed=12093376;
RA      Haas B.U., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA      Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT      "Full-length messenger RNA sequences greatly improve genome
RT      annotation.";
RL      Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN      [2]
RP      SEQUENCE FROM N.A.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 07:29:54 ; Search time 42 Seconds
(without alignments)

650.513 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNYKKMLLSLIGTSTSEF.....LSISVATRLAQDPAPASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgm2_6/prodata/1/iaa/5B_COMB.pep:*
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5: /cgm2_6/prodata/1/iaa/PCUTS_COMB.pep:*
6: /cgm2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------------------------|
| 1 | 1865 | 100.0 | 366 | 4 | US-09-755-6308-247 Sequence 247, App |
| 2 | 1865 | 100.0 | 366 | 4 | US-09-755-274-21 Sequence 21, Appl |
| 3 | 1865 | 100.0 | 389 | 4 | US-09-755-6308-271 Sequence 271, App |
| 4 | 1865 | 100.0 | 389 | 4 | US-09-755-274-33 Sequence 33, Appl |
| 5 | 1769 | 94.9 | 389 | 4 | US-09-755-6308-275 Sequence 275, App |
| 6 | 1769 | 94.9 | 389 | 4 | US-09-755-274-35 Sequence 35, Appl |
| 7 | 1753 | 94.0 | 366 | 4 | US-09-755-6308-259 Sequence 259, App |
| 8 | 1753 | 94.0 | 366 | 4 | US-09-755-274-27 Sequence 27, Appl |
| 9 | 1645 | 88.2 | 366 | 4 | US-09-755-6308-251 Sequence 251, App |
| 10 | 1645 | 88.2 | 366 | 4 | US-09-755-274-23 Sequence 23, Appl |
| 11 | 1544 | 82.8 | 366 | 4 | US-09-755-6308-255 Sequence 255, App |
| 12 | 1544 | 82.8 | 366 | 4 | US-09-755-274-25 Sequence 25, Appl |
| 13 | 1480 | 79.4 | 366 | 4 | US-09-755-6308-263 Sequence 263, App |
| 14 | 1480 | 79.4 | 366 | 4 | US-09-755-274-29 Sequence 29, Appl |
| 15 | 1139 | 61.1 | 367 | 4 | US-09-755-6308-7 Sequence 7, Appl |
| 16 | 1139 | 61.1 | 367 | 4 | US-09-755-274-41 Sequence 41, Appl |
| 17 | 1139 | 61.1 | 386 | 4 | US-09-755-6308-1 Sequence 1, Appl |
| 18 | 1139 | 61.1 | 386 | 4 | US-09-755-6308-265 Sequence 265, App |
| 19 | 1139 | 61.1 | 386 | 4 | US-09-755-6308-286 Sequence 286, App |
| 20 | 1139 | 61.1 | 386 | 4 | US-09-755-274-1 Sequence 1, Appl |
| 21 | 1139 | 61.1 | 386 | 4 | US-09-755-274-31 Sequence 31, Appl |
| 22 | 1139 | 61.1 | 386 | 4 | US-09-755-274-39 Sequence 39, Appl |
| 23 | 1139 | 61.1 | 452 | 4 | US-09-755-6308-6 Sequence 6, Appl |
| 24 | 1139 | 61.1 | 452 | 4 | US-09-755-274-40 Sequence 40, Appl |
| 25 | 1030.5 | 55.3 | 383 | 1 | US-07-936-163-4 Sequence 4, Appl |
| 26 | 1019 | 54.6 | 386 | 4 | US-09-755-6308-279 Sequence 279, App |
| 27 | 1019 | 54.6 | 386 | 4 | US-09-755-274-6 Sequence 6, Appl |

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|----|--------|------|-----|---|--------------------------------------|
| 28 | 1017 | 54.5 | 386 | 4 | US-09-755-6308-278 Sequence 278, App |
| 29 | 1017 | 54.5 | 386 | 4 | US-09-755-274-5 Sequence 5, Appl |
| 30 | 1014 | 54.4 | 381 | 1 | US-07-936-163-3 Sequence 3, Appl |
| 31 | 1014 | 54.4 | 386 | 4 | US-09-755-6308-282 Sequence 282, App |
| 32 | 1014 | 54.4 | 386 | 4 | US-09-755-274-4 Sequence 4, Appl |
| 33 | 1013 | 54.3 | 364 | 4 | US-09-755-6308-281 Sequence 281, App |
| 34 | 1013 | 54.3 | 364 | 4 | US-09-755-274-3 Sequence 3, Appl |
| 35 | 1001.5 | 53.7 | 365 | 4 | US-09-755-6308-280 Sequence 280, App |
| 36 | 1001.5 | 53.7 | 365 | 4 | US-09-755-274-2 Sequence 2, Appl |
| 37 | 528.5 | 28.3 | 408 | 3 | US-09-074-912-2 Sequence 2, Appl |
| 38 | 528.5 | 28.3 | 408 | 3 | US-09-074-912-4 Sequence 4, Appl |
| 39 | 528.5 | 28.3 | 408 | 3 | US-09-290-136-2 Sequence 2, Appl |
| 40 | 528.5 | 28.3 | 408 | 3 | US-09-290-136-4 Sequence 4, Appl |
| 41 | 528.5 | 28.3 | 408 | 4 | US-09-755-6308-287 Sequence 287, App |
| 42 | 528.5 | 28.3 | 408 | 4 | US-09-755-274-7 Sequence 7, Appl |
| 43 | 523 | 28.0 | 410 | 4 | US-09-755-6308-290 Sequence 290, App |
| 44 | 523 | 28.0 | 410 | 4 | US-09-755-274-10 Sequence 10, Appl |
| 45 | 520 | 27.9 | 337 | 4 | US-09-755-6308-293 Sequence 293, App |

ALIGNMENTS

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RESULT 1
US-09-755-6308-247
; Sequence 247, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHIRTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTATIONS
; FILE REFERENCE: 11899.0217, NPUS00 (WOBT217)
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIORITY FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-6308-247

Query Match      100.0%; Score 1865; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.6e-169;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLNYKKMLLSLIGTSTSEFDTYTAKEATWAVHMLVIQKMTDAASYMTDYISTA 60
DB      1 SLNYKKMLLSLIGTSTSEFDTYTAKEATWAVHMLVIQKMTDAASYMTDYISTA 60
QY      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVEENLLKRVSDNDETYEAL 120
DB      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVEENLLKRVSDNDETYEAL 120
QY      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVEENLLKRVSDNDETYEAL 120
DB      61 FOALDSKNNTLYRQENALTTTTEMDASANNELLVQVEENLLKRVSDNDETYEAL 120
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DB      121 KRFKLLSDKRRKLRANKASVGPQLGEMTVLSIDGGGIGIIPATILFLEQLQEMDN 180
QY      181 NADARLADYDVIGTSTGGLTAMISTPENNNRPFPAAYEIVPFYEHGPQJNPSGOI 240
DB      181 NADARLADYDVIGTSTGGLTAMISTPENNNRPFPAAYEIVPFYEHGPQJNPSGOI 240
QY      241 LGRPYDCKYLMQVLOEGLGSTRVHQALETYVISSFDIKTKKPVITFKSNLANSPELDAM 300
DB      241 LGRPYDCKYLMQVLOEGLGSTRVHQALETYVISSFDIKTKKPVITFKSNLANSPELDAM 300
QY      301 YDISYTAAPATYFPFPHYFTVNTNSGDVEYFNLDGAVATVADPALISVATRLAQKDP 360
DB      301 YDISYTAAPATYFPFPHYFTVNTNSGDVEYFNLDGAVATVADPALISVATRLAQKDP 360
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Db 301 YDISYSTAAAPTYFPFPHYFTVNTNSGDEYFENLVDAVAATVADPALLISVATRLAQKDP 360
QY 361 AFASIR 366
Db 361 AFASIR 366

RESULT 2

US-09-755-274-21
; Sequence 21, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755,274
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 21
; LENGTH: 366
; TYPE: PRT
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: Protein
; LOCATION: (1)..(366)
; OTHER INFORMATION: Permutin protein encoded from pMON37402 sequence
US-09-755-274-21

Query Match 100.0%; Score 1865; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.6e-169;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 60
Db 1 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 60
QY 61 FOALDSKNNYLRQVENALTGTTTMDASANNELLVQVGENLLKRPVSEDNPEYTEAL 120
Db 61 FOALDSKNNYLRQVENALTGTTTMDASANNELLVQVGENLLKRPVSEDNPEYTEAL 120
QY 121 KRFKLLSDRKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 180
Db 121 KRFKLLSDRKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 180
QY 181 NADARLADYFDVIGTSTGGLTAMISTPENNNRPPAAKEIYPFYEFGPQIFNPSGQI 240
Db 181 NADARLADYFDVIGTSTGGLTAMISTPENNNRPPAAKEIYPFYEFGPQIFNPSGQI 240
QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 300
Db 241 LGPKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 300
QY 301 YDISYSTAAAPTYFPFPHYFTVNTNSGDEYFENLVDAVAATVADPALLISVATRLAQKDP 360
Db 301 YDISYSTAAAPTYFPFPHYFTVNTNSGDEYFENLVDAVAATVADPALLISVATRLAQKDP 360
QY 361 AFASIR 366
Db 361 AFASIR 366

RESULT 3

US-09-755-630B-271
; Sequence 271, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza F.
; APPLICANT: Astwood, James D.
; APPLICANT: Sampson, Hugh A.
; APPLICANT: McWhorter, Charles A.

; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
; FILE REFERENCE: 11899.0217.NPUS00 (KOB1217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 271
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-271

Query Match 100.0%; Score 1865; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.7e-169;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 60
Db 24 SLNYKKMLLSIGTGTSEFDKTYTAKEATWTAHVHMLVIOKMTDAASSYMTDYILSTA 83
QY 61 FOALDSKNNYLRQVENALTGTTTMDASANNELLVQVGENLLKRPVSEDNPEYTEAL 120
Db 84 FOALDSKNNYLRQVENALTGTTTMDASANNELLVQVGENLLKRPVSEDNPEYTEAL 143
QY 121 KRFKLLSDRKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 180
Db 144 KRFKLLSDRKLRANKASYGPGQLGEMTVLSIDGGIRGIIPATLLEFLBQLOEMDN 203
QY 181 NADARLADYFDVIGTSTGGLTAMISTPENNNRPPAAKEIYPFYEFGPQIFNPSGQI 240
Db 204 NADARLADYFDVIGTSTGGLTAMISTPENNNRPPAAKEIYPFYEFGPQIFNPSGQI 263
QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 300
Db 264 LGPKYDGKYLMOVLQEKLGSTRVHQAITEVVISFDIKTKNPVIFTKSNLANSPELDAM 323
QY 301 YDISYSTAAAPTYFPFPHYFTVNTNSGDEYFENLVDAVAATVADPALLISVATRLAQKDP 360
Db 324 YDISYSTAAAPTYFPFPHYFTVNTNSGDEYFENLVDAVAATVADPALLISVATRLAQKDP 383
QY 361 AFASIR 366
Db 384 AFASIR 389

RESULT 4

US-09-755-274-33
; Sequence 33, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755,274
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 33
; LENGTH: 389
; TYPE: PRT
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: Protein
; LOCATION: (1)..(389)
; OTHER INFORMATION: Permutin protein encoded by pMON40703 sequence
US-09-755-274-33

Query Match 100.0%; Score 1865; DB 4; Length 389;

Best Local Similarity 100.0%; Pred. No. 1.7e-169;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 SLNYKMLLSIGTSTSEFDKTYTAKEATWTAVHMMVLVIOKMTDAASVMTDYLLSTA 83
QY 61 FQALDSKNNYLRVOENALTGTTTMDASSEANMELLVQGENLLKKPVSEDPETEYEAAL 120
DB 84 FQALDSKNNYLRVOENALTGTTTMDASSEANMELLVQGENLLKKPVSEDPETEYEAAL 143
QY 121 KRFAPKLLSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDN 180
DB 144 KRFAPKLLSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDN 203
QY 181 NADARLADVFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEHGPQIFNPSGQI 240
DB 204 NADARLADVFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEHGPQIFNPSGQI 263
QY 241 LGPKYDGLMOVLQEKGETRVHQALTEVVISPDIKTKNPVIFTKSNLANSPELDACKM 300
DB 264 LGPKYDGLMOVLQEKGETRVHQALTEVVISPDIKTKNPVIFTKSNLANSPELDACKM 323
QY 301 YDISYSTAAAPTYFPFHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXP 360
DB 324 YDISYSTAAAPTYFPFHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXP 383
QY 361 APASIR 366
DB 384 APASIR 389
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RESULT 5

US-09-755-630B-275
; Sequence 275, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630B
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 275
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-275

Query Match 94.9%; Score 1769; DB 4; Length 389;
Best Local Similarity 96.7%; Pred. No. 2.5e-160;
Matches 348; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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QY 7 MLLSIGTSTSEFDKTYTAKEATWTAVHMMVLVIOKMTDAASVMTDYLLSTAFAQLDS 66
DB 8 LILIFMILATTSSTPATYTAKEATWTAVHMMVLVIOKMTDAASVMTDYLLSTAFAQLDS 67
QY 67 KNNYLVRVOENALTGTTTMDASSEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPK 126
DB 68 KNNYLVRVOENALTGTTTMDASSEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPK 127
QY 127 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 186
DB 128 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 187
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QY 187 ADVFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEHGPQIFNPSGQILGPKXD 246
DB 188 ADVFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEHGPQIFNPSGQILGPKXD 247
QY 247 GKTIQVLOEKGETRVHQALTEVVISPDIKTKNPVIFTKSNLANSPELDACKYDYSYS 306
DB 248 GKTIQVLOEKGETRVHQALTEVVISPDIKTKNPVIFTKSNLANSPELDACKYDYSYS 307
QY 307 TAAAPTYFPFHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 366
DB 308 TAAAPTYFPFHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 367
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RESULT 6

US-09-755-274-35
; Sequence 35, Application US/09755274
; Patent No. 6657046
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydroxylases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/09/755,274
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 35
; LENGTH: 389
; TYPE: PRT
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: Protein
; LOCATION: (1)..(389)
; OTHER INFORMATION: Permuttein protein encoded by PMON40705
US-09-755-274-35

Query Match 94.9%; Score 1769; DB 4; Length 389;
Best Local Similarity 96.7%; Pred. No. 2.5e-160;
Matches 348; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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QY 7 MLLSIGTSTSEFDKTYTAKEATWTAVHMMVLVIOKMTDAASVMTDYLLSTAFAQLDS 66
DB 8 LILIFMILATTSSTPATYTAKEATWTAVHMMVLVIOKMTDAASVMTDYLLSTAFAQLDS 67
QY 67 KNNYLVRVOENALTGTTTMDASSEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPK 126
DB 68 KNNYLVRVOENALTGTTTMDASSEANMELLVQGENLLKKPVSEDPETEYEAALKRFAPK 127
QY 127 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 186
DB 128 LSDRKKLRANKASYGPGQIGEMVTVLISIDGGIRGIIIPATILFELGQLOEMDNADARL 187
QY 187 ADVFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEHGPQIFNPSGQILGPKXD 246
DB 188 ADVFDVIGTSTGGLLTAMISTPENNNRPPAAKEIVPFYFEHGPQIFNPSGQILGPKXD 247
QY 247 GKTIQVLOEKGETRVHQALTEVVISPDIKTKNPVIFTKSNLANSPELDACKYDYSYS 306
DB 248 GKTIQVLOEKGETRVHQALTEVVISPDIKTKNPVIFTKSNLANSPELDACKYDYSYS 307
QY 307 TAAAPTYFPFHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 366
DB 308 TAAAPTYFPFHYFVNTNSNGDEYEFNLVDGAVATVADPALLISVATRLAQKXPAPASIR 367
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RESULT 7

US-09-755-630B-259
; Sequence 259, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.

APPLICANT: McHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTEDS
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
CURRENT APPLICATION NUMBER: US/09/755,630B
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 295
SOFTWARE: PatentIn version 3.0
SEQ ID NO 259
LENGTH: 366
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-259

Query Match 94.0%; Score 1753; DB 4; Length 366;
Best Local Similarity 99.7%; Pred. No. 7.7e-159; Indels 0; Gaps 0;
Matches 343; Conservative 1; Mismatches 0;

QY 23 TYTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTAFQALDSKNNYLRVOENALTGTT 82
DB 1 TYTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTAFQALDSKNNYLRVOENALTGTT 60
QY 83 TEMDDASEANMELLVQVGENLLKKPVSEDPETYEALRRFAKLLSDRKKLRANKASYGP 142
DB 61 TEMDDASEANMELLVQVGENLLKKPVSEDPETYEALRRFAKLLSDRKKLRANKASYGP 120
QY 143 GOLGEMVTVLSIDGGIRGIIIPATILIEFLGOLQEMDNADRLADYFVIGTSTGGL 202
DB 121 GOLGEMVTVLSIDGGIRGIIIPATILIEFLGOLQEMDNADRLADYFVIGTSTGGL 180
QY 203 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPYDGKYLMOVLQEKLGTR 262
DB 181 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPYDGKYLMOVLQEKLGTR 240
QY 263 VHQALTEVVISFDIKTNKPVIFTKSNLANSPELDKMDISYSTAAAPTYPPHYFTN 322
DB 241 VHQALTEVVISFDIKTNKPVIFTKSNLANSPELDKMDISYSTAAAPTYPPHYFTN 300
QY 323 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
DB 301 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 344

RESULT 8
US-09-755-274-27
Sequence 27, Application US/09755274
Patent No. 6657046
GENERAL INFORMATION:
APPLICANT: Alibhai, Murtaza
APPLICANT: Rydel, Timothy
TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
FILE REFERENCE: 38-21 (51842)B
CURRENT APPLICATION NUMBER: US/09/755,274
CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 366
TYPE: PRT
ORGANISM: synthetic
FEATURE:
NAME/KEY: Protein
LOCATION: (1)..(366)
OTHER INFORMATION: Permutated protein encoded by pMON37407 sequence
US-09-755-274-27

Query Match 94.0%; Score 1753; DB 4; Length 366;
Best Local Similarity 99.7%; Pred. No. 7.7e-159; Indels 0; Gaps 0;
Matches 343; Conservative 1; Mismatches 0;

QY 23 TYTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTAFQALDSKNNYLRVOENALTGTT 82
DB 1 TYTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTAFQALDSKNNYLRVOENALTGTT 60
QY 83 TEMDDASEANMELLVQVGENLLKKPVSEDPETYEALRRFAKLLSDRKKLRANKASYGP 142
DB 61 TEMDDASEANMELLVQVGENLLKKPVSEDPETYEALRRFAKLLSDRKKLRANKASYGP 120
QY 143 GOLGEMVTVLSIDGGIRGIIIPATILIEFLGOLQEMDNADRLADYFVIGTSTGGL 202
DB 121 GOLGEMVTVLSIDGGIRGIIIPATILIEFLGOLQEMDNADRLADYFVIGTSTGGL 180
QY 203 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPYDGKYLMOVLQEKLGTR 262
DB 181 TMIISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQILGPYDGKYLMOVLQEKLGTR 240
QY 263 VHQALTEVVISFDIKTNKPVIFTKSNLANSPELDKMDISYSTAAAPTYPPHYFTN 322
DB 241 VHQALTEVVISFDIKTNKPVIFTKSNLANSPELDKMDISYSTAAAPTYPPHYFTN 300
QY 323 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
DB 301 TSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 344

RESULT 9
US-09-755-630B-251
Sequence 251, Application US/09755630B
Patent No. 6639054
GENERAL INFORMATION:
APPLICANT: ALIBHAI, MURTAZA F.
APPLICANT: ASTWOOD, JAMES D.
APPLICANT: CAMPSON, HUGH A.
APPLICANT: McHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTEDS
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
CURRENT APPLICATION NUMBER: US/09/755,630B
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 295
SOFTWARE: PatentIn version 3.0
SEQ ID NO 251
LENGTH: 366
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-251

Query Match 88.2%; Score 1645; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.6e-148; Indels 0; Gaps 0;
Matches 321; Conservative 0; Mismatches 0;

QY 1 SLNYKKMLLSIGTGTSTSEFDKTYTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTA 60
DB 46 SLNYKKMLLSIGTGTSTSEFDKTYTAKAAATWTAVHMLVIOKMTDAASSYMTDYLLSTA 105
QY 61 FOALDSKNNYLRVOENALTGTTTEMDDASEANMELLVQVGENLLKKPVSEDPETYEAL 120
DB 106 FOALDSKNNYLRVOENALTGTTTEMDDASEANMELLVQVGENLLKKPVSEDPETYEAL 165
QY 121 KRPAKLLSDRKKLRANKASYGPQOLGEMVTVLSIDGGIRGIIIPATILIEFLGOLQEMDN 180
DB 166 KRPAKLLSDRKKLRANKASYGPQOLGEMVTVLSIDGGIRGIIIPATILIEFLGOLQEMDN 225
QY 181 NADARLADYFVIGTSTGGLTAMISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQI 240
DB 226 NADARLADYFVIGTSTGGLTAMISTPNNRNPFAAKEIVPFYFHEGPOIFNPSSQI 285
QY 241 LQPKYDGKYLMOVLQEKLGTRVHQALTEVVISFDIKTNKPVIFTKSNLANSPELDKMD 300
DB 286 LQPKYDGKYLMOVLQEKLGTRVHQALTEVVISFDIKTNKPVIFTKSNLANSPELDKMD 345

QY 301 YDISYSTAAAPTYPPHYFT 321
Db 346 YDISYSTAAAPTYPPHYFT 366

RESULT 10

US-09-755-274-23
Sequence 23, Application US/09755274

Patent No. 6657046

GENERAL INFORMATION:

APPLICANT: Alibhai, Murtaza

APPLICANT: Rydel, Timothy

TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases

FILE REFERENCE: 38-21 (51842)B

CURRENT APPLICATION NUMBER: US/09/755,274

CURRENT FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.0

SEQ ID NO 23

LENGTH: 366

TYPE: PRT

ORGANISM: synthetic

FEATURE:

NAME/KEY: Protein

LOCATION: (1)..(366)

OTHER INFORMATION: Permutin protein encoded by pMON37405 sequence

US-09-755-274-23

Query Match 82.8%; Score 1645; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 1.6e-148;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEPDKTYTAAATWAVHMLVIQKWTDAASSYMTDYISTA 60

Db 46 SLNYKKMLLSLGTGTTSEPDKTYTAAATWAVHMLVIQKWTDAASSYMTDYISTA 105

QY 61 FOALDSKNNTLRVQENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYEEAL 120

Db 106 FOALDSKNNTLRVQENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYEEAL 165

QY 121 KRPAKLSDRKKLRANKASYGPGQIGEMTVLSIDGGIRIGIIPATLLEFLEQLOEMDN 180

Db 166 KRPAKLSDRKKLRANKASYGPGQIGEMTVLSIDGGIRIGIIPATLLEFLEQLOEMDN 225

QY 181 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYEHGPQIFNPSGOI 240

Db 226 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYEHGPQIFNPSGOI 285

QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 300

Db 286 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 345

QY 301 YDISYSTAAAPTYPPHYFT 321

Db 346 YDISYSTAAAPTYPPHYFT 366

RESULT 11

US-09-755-630B-255

Sequence 255, Application US/09755630B

Patent No. 6639054

GENERAL INFORMATION:

APPLICANT: Alibhai, Murtaza F.

APPLICANT: ASTWOOD, JAMES D.

APPLICANT: SAMPSON, HUGH A.

APPLICANT: MCHESTER, CHARLES A.

TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS

FILE REFERENCE: 11899 0217.NPUS00 (MOBT217)

CURRENT APPLICATION NUMBER: US/09/755,630B

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 60/174,669

PRIOR FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 295
SOFTWARE: Patentin version 3.0
SEQ ID NO 255
LENGTH: 366

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic polypeptide

US-09-755-630B-255

Query Match 82.8%; Score 1544; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 6.9e-139;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEPDKTYTAAATWAVHMLVIQKWTDAASSYMTDYISTA 60

Db 64 SLNYKKMLLSLGTGTTSEPDKTYTAAATWAVHMLVIQKWTDAASSYMTDYISTA 123

QY 61 FOALDSKNNTLRVQENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYEEAL 120

Db 124 FOALDSKNNTLRVQENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYEEAL 183

QY 121 KRPAKLSDRKKLRANKASYGPGQIGEMTVLSIDGGIRIGIIPATLLEFLEQLOEMDN 180

Db 184 KRPAKLSDRKKLRANKASYGPGQIGEMTVLSIDGGIRIGIIPATLLEFLEQLOEMDN 243

QY 181 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYEHGPQIFNPSGOI 240

Db 244 NADARLADYFDVIGSTGGLTAMISTPENNNRPFAAAEIVPFYEHGPQIFNPSGOI 303

QY 241 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 300

Db 304 LGPKYDGKYLMOVLQEKLGSTRVHQALTEVVISFDIKTKNPVIFTKSNLANSPELDAM 363

QY 301 YDI 303

Db 364 YDI 366

RESULT 12

US-09-755-274-25

Sequence 25, Application US/09755274

Patent No. 6657046

GENERAL INFORMATION:

APPLICANT: Alibhai, Murtaza

APPLICANT: Rydel, Timothy

TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases

FILE REFERENCE: 38-21 (51842)B

CURRENT APPLICATION NUMBER: US/09/755,274

CURRENT FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.0

SEQ ID NO 25

LENGTH: 366

TYPE: PRT

ORGANISM: synthetic

FEATURE:

NAME/KEY: Protein

LOCATION: (1)..(366)

OTHER INFORMATION: Permutin protein encoded by pMON37406

US-09-755-274-25

Query Match 82.8%; Score 1544; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 6.9e-139;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLNYKKMLLSLGTGTTSEPDKTYTAAATWAVHMLVIQKWTDAASSYMTDYISTA 60

Db 64 SLNYKKMLLSLGTGTTSEPDKTYTAAATWAVHMLVIQKWTDAASSYMTDYISTA 123

QY 61 FOALDSKNNTLRVQENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYEEAL 120

Db 124 FOALDSKNNTLRVQENALTGTTEMDASEANMELLVQVGENLLKRVSEDNPEYEEAL 183

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|----|-----|---|-----|
| Db | 5 | QJGEMWTVLSIDGGIRGIIIPATIEFLEGOJQEMDNADARLADYFDVIGTSGGLT | 64 |
| Qy | 204 | AMISTPENENRPPAAAKEIVPFYFEHGPQIFNPSGOILGPKYDKYLMQVLOEKLGSTRV | 263 |
| Db | 65 | AMISTPENENRPPAAAKEIVPFYFEHGPQIFNPSGOILGPKYDKYLMQVLOEKLGSTRV | 124 |
| Qy | 264 | HOALTEVVISSPDIKTNKPVIFTKSNLANSPELDKAYDISYSTAAPTYFPHYFVTNT | 323 |
| Db | 125 | HOALTEVVISSPDIKTNKPVIFTKSNLANSPELDKAYDISYSTAAPTYFPHYFVTNT | 184 |
| Qy | 324 | SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR | 366 |
| Db | 185 | SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR | 227 |

Search completed: April 8, 2005, 07:57:52
 Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 07:56:20 ; Search time 55 Seconds
(without alignments)
2209.291 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNYKKMLLSLGTGTSEF.....LSISVATRLAQKPAPASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubppa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1 | 1865 | 100.0 | 366 | 10 | US-09-755-630A-247 Sequence 247, App |
| 2 | 1865 | 100.0 | 366 | 10 | US-09-755-630A-271 Sequence 271, App |
| 3 | 1769 | 94.9 | 366 | 10 | US-09-755-630A-275 Sequence 275, App |
| 4 | 1753 | 94.0 | 366 | 10 | US-09-755-630A-259 Sequence 259, App |
| 5 | 1645 | 88.2 | 366 | 10 | US-09-755-630A-251 Sequence 251, App |
| 6 | 1544 | 82.8 | 366 | 10 | US-09-755-630A-255 Sequence 255, App |
| 7 | 1480 | 79.4 | 366 | 10 | US-09-755-630A-263 Sequence 263, App |
| 8 | 1139 | 61.1 | 366 | 10 | US-09-755-630A-7 Sequence 7, App1 |
| 9 | 1139 | 61.1 | 366 | 10 | US-09-755-630A-2 Sequence 2, App1 |
| 10 | 1139 | 61.1 | 366 | 10 | US-09-755-630A-265 Sequence 265, App |
| 11 | 1139 | 61.1 | 366 | 10 | US-09-755-630A-286 Sequence 286, App |
| 12 | 1139 | 61.1 | 452 | 10 | US-09-755-630A-6 Sequence 6, App1 |
| 13 | 1019 | 54.6 | 366 | 10 | US-09-755-630A-279 Sequence 279, App |

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| 14 | 1017 | 54.5 | 386 | 10 | US-09-755-630A-278 Sequence 278, App |
| 15 | 1014 | 54.4 | 386 | 10 | US-09-755-630A-282 Sequence 282, App |
| 16 | 1013 | 54.3 | 364 | 10 | US-09-755-630A-281 Sequence 281, App |
| 17 | 1001.5 | 53.7 | 365 | 10 | US-09-755-630A-280 Sequence 280, App |
| 18 | 618.5 | 33.2 | 335 | 15 | US-10-424-599-143308 Sequence 143308, App |
| 19 | 609.5 | 32.7 | 405 | 16 | US-10-437-963-129647 Sequence 129647, App |
| 20 | 585 | 31.4 | 387 | 16 | US-10-437-963-177823 Sequence 177823, App |
| 21 | 579 | 31.0 | 400 | 14 | US-10-150-4298-1 Sequence 1, App1 |
| 22 | 565.5 | 30.3 | 438 | 15 | US-10-425-114-72032 Sequence 72032, A |
| 23 | 565.5 | 30.3 | 438 | 15 | US-10-425-114-72035 Sequence 72035, A |
| 24 | 565.5 | 30.3 | 448 | 15 | US-10-425-114-65072 Sequence 65072, A |
| 25 | 545 | 29.2 | 442 | 16 | US-10-437-963-138254 Sequence 138254, App |
| 26 | 545 | 29.2 | 1275 | 16 | US-10-437-963-199835 Sequence 199835, App |
| 27 | 544.5 | 29.2 | 431 | 16 | US-10-437-963-108232 Sequence 108232, App |
| 28 | 537.5 | 28.8 | 430 | 16 | US-10-437-963-109130 Sequence 109130, App |
| 29 | 534.5 | 28.7 | 390 | 14 | US-10-034-937-4 Sequence 4, App1 |
| 30 | 534.5 | 28.7 | 390 | 14 | US-10-034-937-10 Sequence 10, App1 |
| 31 | 533 | 28.6 | 390 | 14 | US-10-034-937-12 Sequence 12, App1 |
| 32 | 531.5 | 28.5 | 390 | 14 | US-10-034-937-38 Sequence 38, App1 |
| 33 | 529.5 | 28.4 | 390 | 14 | US-10-034-937-8 Sequence 8, App1 |
| 34 | 528.5 | 28.3 | 387 | 14 | US-10-034-937-42 Sequence 42, App1 |
| 35 | 528.5 | 28.3 | 390 | 14 | US-10-034-937-16 Sequence 16, App1 |
| 36 | 528.5 | 28.3 | 390 | 14 | US-10-034-937-20 Sequence 20, App1 |
| 37 | 528.5 | 28.3 | 390 | 14 | US-10-034-937-32 Sequence 32, App1 |
| 38 | 528.5 | 28.3 | 390 | 14 | US-10-034-937-34 Sequence 34, App1 |
| 39 | 528.5 | 28.3 | 390 | 14 | US-10-034-937-41 Sequence 41, App1 |
| 40 | 528.5 | 28.3 | 407 | 14 | US-10-034-937-43 Sequence 43, App1 |
| 41 | 528.5 | 28.3 | 408 | 10 | US-09-755-630A-287 Sequence 287, App |
| 42 | 528.5 | 28.3 | 477 | 16 | US-10-437-963-137697 Sequence 137697, App1 |
| 43 | 527.5 | 28.3 | 390 | 14 | US-10-034-937-6 Sequence 6, App1 |
| 44 | 527 | 28.3 | 386 | 14 | US-10-034-937-2 Sequence 2, App1 |
| 45 | 527 | 28.3 | 390 | 14 | US-10-034-937-22 Sequence 22, App1 |

ALIGNMENTS

RESULT 1
US-09-755-630A-247
; Sequence 247, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALTBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMOTELINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-247
Query Match 100.0%; Score 1865; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 2.7e-157;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLNYKKMLLSLGTGTSEFDTYTAKEATWTAVHMLVYQKWTDAASMYDDYVSTA 60
DB 1 SLNYKKMLLSLGTGTSEFDTYTAKEATWTAVHMLVYQKWTDAASMYDDYVSTA 60
QY 61 FOALDSKNYILRVOENALTGTTTMDASANNELLVQVGENLLKRPVSDNPETYEAL 120
DB 61 FOALDSKNYILRVOENALTGTTTMDASANNELLVQVGENLLKRPVSDNPETYEAL 120

;; CURRENT FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 60/174,669
;; PRIOR FILING DATE: 2000-01-06
;; NUMBER OF SEQ ID NOS: 293
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO 259
;; LENGTH: 366
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-259

Query Match 94.0%; Score 1753; DB 10; Length 366;
Best Local Similarity 99.7%; Pred. No. 2.5e-147;
Matches 343; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 TYTAKAATWTAVHMLVIOKMTDAASMYTDYLLSTAFOALDSKNNYLKVOENALTGTT 82
DB 1 TYTAKAATWTAVHMLVIOKMTDAASMYTDYLLSTAFOALDSKNNYLKVOENALTGTT 60
QY 83 TEMDDASEANMELLVOGENLLKKPVSEDPETYEELKRFACLLSDRKKLRANKASYCP 142
DB 61 TEMDDASEANMELLVOGENLLKKPVSEDPETYEELKRFACLLSDRKKLRANKASYCP 120
QY 143 GOLGEVTVLSDGGIRGIIIPATILFLEGOLOEMDNADRLADYFDVIGTSTGGIL 202
DB 121 GOLGEVTVLSDGGIRGIIIPATILFLEGOLOEMDNADRLADYFDVIGTSTGGIL 180
QY 203 TAMISTPNNRPPFAAKEIYPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLETR 262
DB 181 TAMISTPNNRPPFAAKEIYPFYFEHGPQIFNPSGQILGPKYDGKYLMOVLQEKLETR 240
QY 263 VHOALTEVVISFDIKTKNPVITKSNLANSPELDAMVDISYTAAPTYFPPHYFTVN 322
DB 241 VHOALTEVVISFDIKTKNPVITKSNLANSPELDAMVDISYTAAPTYFPPHYFTVN 300
QY 323 TSNGDEYEFNVDGAVATVADPALLSISVATRLAODPAPASIR 366
DB 301 TSNGDEYEFNVDGAVATVADPALLSISVATRLAODPAPASIR 344

RESULT 5
US-09-755-630A-251
;; Sequence 251, Application US/09755630A
;; Publication No. US20030194399A1
;; GENERAL INFORMATION:
;; APPLICANT: ALIBHAI, MURTAZA F.
;; APPLICANT: ASTWOOD, JAMES D.
;; APPLICANT: SAMPSON, HUGH A.
;; APPLICANT: MCMHERTER, CHARLES A.
;; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTATEINS
;; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
;; CURRENT APPLICATION NUMBER: US/09/755,630A
;; CURRENT FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 60/174,669
;; PRIOR FILING DATE: 2000-01-06
;; NUMBER OF SEQ ID NOS: 293
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO 251
;; LENGTH: 366
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-251

Query Match 88.2%; Score 1645; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 1e-137;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASMYTDYLLSTA 60
DB 1 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASMYTDYLLSTA 60

DB 46 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASMYTDYLLSTA 105
QY 61 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENLLKKPVSEDPETYEEL 120
DB 106 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENLLKKPVSEDPETYEEL 165
QY 121 KRPAKLLSDRKKLRANKASYGPGQLEGEMTVLSDGGIRGIIIPATILFLEGOLOEMDN 180
DB 166 KRPAKLLSDRKKLRANKASYGPGQLEGEMTVLSDGGIRGIIIPATILFLEGOLOEMDN 225
QY 181 MADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIYPFYFEHGPQIFNPSGQI 240
DB 226 MADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIYPFYFEHGPQIFNPSGQI 285
QY 241 LGPKYDGKYLMOVLQEKLETRVHOALTEVVISFDIKTKNPVITKSNLANSPELDAM 300
DB 286 LGPKYDGKYLMOVLQEKLETRVHOALTEVVISFDIKTKNPVITKSNLANSPELDAM 345
QY 301 YDISYSTAAAPTYFPPHYFTV 321
DB 346 YDISYSTAAAPTYFPPHYFTV 366

RESULT 6
US-09-755-630A-255
;; Sequence 255, Application US/09755630A
;; Publication No. US20030194399A1
;; GENERAL INFORMATION:
;; APPLICANT: ALIBHAI, MURTAZA F.
;; APPLICANT: ASTWOOD, JAMES D.
;; APPLICANT: SAMPSON, HUGH A.
;; APPLICANT: MCMHERTER, CHARLES A.
;; TITLE OF INVENTION: PREPARATION OF DEALTERGENIZED PROTEINS AND PERMUTATEINS
;; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
;; CURRENT APPLICATION NUMBER: US/09/755,630A
;; CURRENT FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 60/174,669
;; PRIOR FILING DATE: 2000-01-06
;; NUMBER OF SEQ ID NOS: 293
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO 255
;; LENGTH: 366
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-255

Query Match 82.8%; Score 1544; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASMYTDYLLSTA 60
DB 64 SLNYKKMLLSLGTGTTSEFDKTYTAKAATWTAVHMLVIOKMTDAASMYTDYLLSTA 123
QY 61 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENLLKKPVSEDPETYEEL 120
DB 124 FOALDSKNNYLKVOENALGTTTEMDDASEANMELLVOGENLLKKPVSEDPETYEEL 163
QY 121 KRPAKLLSDRKKLRANKASYGPGQLEGEMTVLSDGGIRGIIIPATILFLEGOLOEMDN 180
DB 184 KRPAKLLSDRKKLRANKASYGPGQLEGEMTVLSDGGIRGIIIPATILFLEGOLOEMDN 243
QY 181 MADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIYPFYFEHGPQIFNPSGQI 240
DB 244 MADARLADYFDVIGTSTGGILTAMISTPNNRPPFAAKEIYPFYFEHGPQIFNPSGQI 303
QY 241 LGPKYDGKYLMOVLQEKLETRVHOALTEVVISFDIKTKNPVITKSNLANSPELDAM 300
DB 304 LGPKYDGKYLMOVLQEKLETRVHOALTEVVISFDIKTKNPVITKSNLANSPELDAM 363
QY 301 YDI 303

Db 364 YDI 366

RESULT 7
US-09-755-630A-263

Sequence 263, Application US/09755630A
Publication No. US20030194399A1
GENERAL INFORMATION:
APPLICANT: ALIBHAI, MURTAZA F.
APPLICANT: ASTWOOD, JAMES D.
APPLICANT: SAMPOON, HUGH A.
APPLICANT: MCHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
CURRENT APPLICATION NUMBER: US/09/755,630A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 293
SOFTWARE: PatentIn version 3.0
SEQ ID NO 263
LENGTH: 366
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-263

Query Match 79.4%; Score 1480; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 5e-123;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 76 NATGGTTEMDDESEANMELLVOYGENLLKKPVSEDPETTYEALKKFAKLISDRKKLRA 135
1 NATGGTTEMDDESEANMELLVOYGENLLKKPVSEDPETTYEALKKFAKLISDRKKLRA 60
QY 136 NKASYGFGQGEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGG 195
Db 61 NKASYGFGQGEWTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGG 120
QY 196 TSGGGLTAMISTPENNRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQ 255
Db 121 TSGGGLTAMISTPENNRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQ 180
QY 256 EKGTEHVHQAITEVVISFSDIKTKKPVIFTKSNLANSPELDAMVDISYTAAPTYFP 315
Db 181 EKGTEHVHQAITEVVISFSDIKTKKPVIFTKSNLANSPELDAMVDISYTAAPTYFP 240
QY 316 PHYFVNTSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
Db 241 PHYFVNTSNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 291

RESULT 8

US-09-755-630A-7
Sequence 7, Application US/09755630A
Publication No. US20030194399A1
GENERAL INFORMATION:
APPLICANT: ALIBHAI, MURTAZA F.
APPLICANT: ASTWOOD, JAMES D.
APPLICANT: SAMPOON, HUGH A.
APPLICANT: MCHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
CURRENT APPLICATION NUMBER: US/09/755,630A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 293
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 367

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-7

Query Match 61.1%; Score 1139; DB 10; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 QLGEMVTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGTSTGGLT 203
Db 5 QLGEMVTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGTSTGGLT 64
QY 204 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRY 263
Db 65 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRY 124
QY 264 HQALTEVVISFSDIKTKKPVIFTKSNLANSPELDAMVDISYTAAPTYFPFHYFVNT 323
Db 125 HQALTEVVISFSDIKTKKPVIFTKSNLANSPELDAMVDISYTAAPTYFPFHYFVNT 184
QY 324 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
Db 185 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 227

RESULT 9
US-09-755-630A-2

Sequence 2, Application US/09755630A
Publication No. US20030194399A1
GENERAL INFORMATION:
APPLICANT: ALIBHAI, MURTAZA F.
APPLICANT: ASTWOOD, JAMES D.
APPLICANT: SAMPOON, HUGH A.
APPLICANT: MCHERTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTINS
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
CURRENT APPLICATION NUMBER: US/09/755,630A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 293
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 386
TYPE: PRT
ORGANISM: Solanum tuberosum
US-09-755-630A-2

Query Match 61.1%; Score 1139; DB 10; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 QLGEMVTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGTSTGGLT 203
Db 24 QLGEMVTVLSIDGGIRGIIIPATILEFLEGQLOEMDNADALADYFDVIGTSTGGLT 83
QY 204 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRY 263
Db 84 AMISTENNRRPFAAKEIVPFYFEGPOIFNPSGQILGPKYDGLMOVLQEKLETRY 143
QY 264 HQALTEVVISFSDIKTKKPVIFTKSNLANSPELDAMVDISYTAAPTYFPFHYFVNT 323
Db 144 HQALTEVVISFSDIKTKKPVIFTKSNLANSPELDAMVDISYTAAPTYFPFHYFVNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 366
Db 204 SNGDEYEFNLVDGAVATVADPALLSISVATRLAQKDPAPASIR 246

RESULT 10
US-09-755-630A-265

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; Sequence 265, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 265
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-265
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Query Match 61.1%; Score 1139; DB 10; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 144 QLGEMTVLISIDGGIRGIIIPATILFELEGQLOEMDNADARLADYDVIGTSTGGLT 203
DB 24 QLGEMTVLISIDGGIRGIIIPATILFELEGQLOEMDNADARLADYDVIGTSTGGLT 83
QY 204 AMISTENNRRPFAAKEIYVFFEHGPQIFNPSGQILGPKYDKYLMQVLOEKLGETRV 263
DB 84 AMISTENNRRPFAAKEIYVFFEHGPQIFNPSGQILGPKYDKYLMQVLOEKLGETRV 143
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPPHYFTNT 323
DB 144 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPPHYFTNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 366
DB 204 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 246
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```
RESULT 11
US-09-755-630A-286
; Sequence 286, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 286
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-755-630A-286
```

```
Query Match 61.1%; Score 1139; DB 10; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 QLGEMTVLISIDGGIRGIIIPATILFELEGQLOEMDNADARLADYDVIGTSTGGLT 203
DB 24 QLGEMTVLISIDGGIRGIIIPATILFELEGQLOEMDNADARLADYDVIGTSTGGLT 83
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DB 24 QLGEMTVLISIDGGIRGIIIPATILFELEGQLOEMDNADARLADYDVIGTSTGGLT 83
QY 204 AMISTENNRRPFAAKEIYVFFEHGPQIFNPSGQILGPKYDKYLMQVLOEKLGETRV 263
DB 84 AMISTENNRRPFAAKEIYVFFEHGPQIFNPSGQILGPKYDKYLMQVLOEKLGETRV 143
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPPHYFTNT 323
DB 144 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPPHYFTNT 203
QY 324 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 366
DB 204 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 246
```

```
RESULT 12
US-09-755-630A-6
; Sequence 6, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-6
```

```
Query Match 61.1%; Score 1139; DB 10; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 144 QLGEMTVLISIDGGIRGIIIPATILFELEGQLOEMDNADARLADYDVIGTSTGGLT 203
DB 90 QLGEMTVLISIDGGIRGIIIPATILFELEGQLOEMDNADARLADYDVIGTSTGGLT 149
QY 204 AMISTENNRRPFAAKEIYVFFEHGPQIFNPSGQILGPKYDKYLMQVLOEKLGETRV 263
DB 150 AMISTENNRRPFAAKEIYVFFEHGPQIFNPSGQILGPKYDKYLMQVLOEKLGETRV 209
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPPHYFTNT 323
DB 210 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDKAKYDISYTAAPTYFPPHYFTNT 269
QY 324 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 366
DB 270 SNGDEYEFNLVDGAVATVADPALISISVATRLAQKDPAPASIR 312
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```
RESULT 13
US-09-755-630A-279
; Sequence 279, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCMHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755.630A
```

;; CURRENT FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 60/174,669
;; PRIOR FILING DATE: 2000-01-06
;; NUMBER OF SEQ ID NOS: 293
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 279
;; LENGTH: 386
;; TYPE: PRT
;; ORGANISM: Solanum tuberosum
US-09-755-630A-279

Query Match 54.6%; Score 1019; DB 10; Length 386;
Best Local Similarity 88.7%; Pred. No. 6e-82;
Matches 197; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 145 IGEWTVLSIDGGIRGIIIPATILEFLEGOLOEMDNADARLADYDVGSTGGLT 204
DB 25 IGEWTVLSIDGGIRGIIIPATILEFLEGOLOEMDNADARLADYDVGSTGGLT 84
QY 205 MISTPENNRPFAAKEIVPFYFEGHPOIFNPSGQILGPKYDGYLMQVLOEKLG 264
DB 85 MISTPENNRPFAAKEIVPFYFEGHPOIFNPSGQILGPKYDGYLMQVLOEKLG 144
QY 265 QALTEVVISFDIKTKNPVIFTKSNLANSPELDAMKWDISYSTRAPTYPPHYFV 324
DB 145 QALTEVVISFDIKTKNPVIFTKSNLAKSPELDAMKWDICYSTAAPTYPPHYFV 204
QY 325 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 205 NGDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 246

RESULT 14
US-09-755-630A-278
;; Sequence 278, Application US/09755630A
;; Publication No. US2003019439A1
;; GENERAL INFORMATION:
;; APPLICANT: ALIBHAI, MURTAZA F.
;; APPLICANT: ASTWOOD, JAMES D.
;; APPLICANT: SAMPSON, HUGH A.
;; APPLICANT: MCMEHTER, CHARLES A.
;; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTTEINS
;; FILE REFERENCE: 11899.0217.NPUS00 (MOB1217)
;; CURRENT APPLICATION NUMBER: US/09/755,630A
;; PRIOR FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 60/174,669
;; NUMBER OF SEQ ID NOS: 293
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 278
;; LENGTH: 386
;; TYPE: PRT
;; ORGANISM: Solanum tuberosum
US-09-755-630A-278

Query Match 54.5%; Score 1017; DB 10; Length 386;
Best Local Similarity 87.9%; Pred. No. 9e-82;
Matches 196; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLEWTVLSIDGGIRGIIIPATILEFLEGOLOEMDNADARLADYDVGSTGGLT 203
DB 24 KLEWTVLSIDGGIRGIIIPATILEFLEGOLOEMDNADARLADYDVGSTGGLT 83
QY 204 AMISTENNRPFAAKEIVPFYFEGHPOIFNPSGQILGPKYDGYLMQVLOEKLG 263
DB 84 AMISTENNRPFAAKEIVPFYFEGHPOIFNPSGQILGPKYDGYLMQVLOEKLG 143
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDAMKWDISYSTRAPTYPPHYFV 323
DB 144 HQALTEVVISFDIKTKNPVIFTKSNLAKSPELDAMKWDICYSTAAPTYPPHYFV 203
QY 324 SNDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366

DB 204 SNDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 246

RESULT 15
US-09-755-630A-282
;; Sequence 282, Application US/09755630A
;; Publication No. US2003019439A1
;; GENERAL INFORMATION:
;; APPLICANT: ALIBHAI, MURTAZA F.
;; APPLICANT: ASTWOOD, JAMES D.
;; APPLICANT: SAMPSON, HUGH A.
;; APPLICANT: MCMEHTER, CHARLES A.
;; TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTTEINS
;; FILE REFERENCE: 11899.0217.NPUS00 (MOB1217)
;; CURRENT APPLICATION NUMBER: US/09/755,630A
;; PRIOR FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 60/174,669
;; NUMBER OF SEQ ID NOS: 293
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 282
;; LENGTH: 386
;; TYPE: PRT
;; ORGANISM: Solanum tuberosum
US-09-755-630A-282

Query Match 54.4%; Score 1014; DB 10; Length 386;
Best Local Similarity 88.3%; Pred. No. 1.7e-81;
Matches 197; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 144 QLEWTVLSIDGGIRGIIIPATILEFLEGOLOEMDNADARLADYDVGSTGGLT 203
DB 24 KLEWTVLSIDGGIRGIIIPATILEFLEGOLOEMDNADARLADYDVGSTGGLT 83
QY 204 AMISTENNRPFAAKEIVPFYFEGHPOIFNPSGQILGPKYDGYLMQVLOEKLG 263
DB 84 AMISTENNRPFAAKEIVPFYFEGHPOIFNPSGQILGPKYDGYLMQVLOEKLG 143
QY 264 HQALTEVVISFDIKTKNPVIFTKSNLANSPELDAMKWDISYSTRAPTYPPHYFV 323
DB 144 HQALTEVVISFDIKTKNPVIFTKSNLAKSPELDAMKWDICYSTAAPTYPPHYFV 203
QY 324 SNDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 366
DB 204 SNDEYEFNLVDGAVATVADPALISVATRLAQKDPAPASIR 246

Search completed: April 8, 2005, 08:10:38
Job time : 56 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 07:38:59 ; Search time 38 Seconds
(without alignments)
631.316 Million cell updates/sec

Title: US-10-658-180-247

Perfect score: 1865

Sequence: 1 SLNKKMLLSLGTTSERF.....LSIVATRLAQDPAPASIR 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 288363 seqs, 65546468 residues

Total number of hits satisfying chosen parameters: 288363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA New:*
1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/prodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--|
| 1 | 1014 | 54.4 | 386 | 7 | US-11-061-894-14 Sequence 14, Appl |
| 2 | 528.5 | 28.3 | 408 | 7 | US-11-061-894-10 Sequence 10, Appl |
| 3 | 528.5 | 28.3 | 408 | 7 | US-11-061-894-12 Sequence 12, Appl |
| 4 | 268.5 | 14.4 | 350 | 1 | PCT-US05-07908-100 Sequence 100, Appl |
| 5 | 242 | 13.0 | 378 | 1 | PCT-US05-07908-18 Sequence 18, Appl |
| 6 | 239.5 | 12.8 | 387 | 1 | PCT-US05-07908-66 Sequence 66, Appl |
| 7 | 234.5 | 12.6 | 308 | 1 | PCT-US05-07908-166 Sequence 166, Appl |
| 8 | 197 | 10.6 | 308 | 1 | PCT-US05-07908-132 Sequence 132, Appl |
| 9 | 165 | 8.8 | 462 | 1 | PCT-US05-07908-36 Sequence 36, Appl |
| 10 | 154 | 8.3 | 364 | 8 | US-60-655-875-130981 Sequence 130981, Appl |
| 11 | 146.5 | 7.9 | 314 | 7 | US-11-061-233-8 Sequence 8, Appl |
| 12 | 146.5 | 7.9 | 314 | 7 | US-11-061-894-8 Sequence 8, Appl |
| 13 | 136.5 | 7.3 | 239 | 8 | US-60-655-875-139557 Sequence 139557, Appl |
| 14 | 133.5 | 7.2 | 258 | 8 | US-60-655-875-127287 Sequence 127287, Appl |
| 15 | 113 | 6.1 | 444 | 7 | US-11-045-874-10 Sequence 10, Appl |
| 16 | 106 | 6.1 | 140 | 8 | US-60-655-875-158378 Sequence 158378, Appl |
| 17 | 105 | 5.6 | 3051 | 1 | PCT-IB03-06509-3039 Sequence 3039, Appl |
| 18 | 104 | 5.6 | 1682 | 6 | US-10-450-763-37598 Sequence 37598, Appl |
| 19 | 104 | 5.6 | 1682 | 6 | US-10-450-763-44026 Sequence 44026, Appl |
| 20 | 104 | 5.6 | 2159 | 6 | US-10-450-763-44023 Sequence 44023, Appl |
| 21 | 104 | 5.6 | 2503 | 6 | US-10-450-763-37597 Sequence 37597, Appl |
| 22 | 104 | 5.6 | 2503 | 6 | US-10-450-763-43913 Sequence 43913, Appl |
| 23 | 104 | 5.6 | 2871 | 6 | US-10-450-763-37602 Sequence 37602, Appl |
| 24 | 104 | 5.6 | 2871 | 6 | US-10-450-763-43914 Sequence 43914, Appl |
| 25 | 104 | 5.6 | 2871 | 6 | US-10-450-763-44024 Sequence 44024, Appl |

| | | | | | |
|----|-------|-----|------|---|---------------------------------------|
| 26 | 104 | 5.6 | 2891 | 6 | US-10-450-763-37599 Sequence 37599, A |
| 27 | 104 | 5.6 | 2891 | 6 | US-10-450-763-43915 Sequence 43915, A |
| 28 | 104 | 5.6 | 2891 | 6 | US-10-450-763-44025 Sequence 44025, A |
| 29 | 103.5 | 5.5 | 399 | 7 | US-11-027-399-3323 Sequence 3323, Ap |
| 30 | 103.5 | 5.5 | 399 | 7 | US-11-027-843-3323 Sequence 3323, Ap |
| 31 | 103.5 | 5.5 | 399 | 7 | US-11-027-878-3323 Sequence 3323, Ap |
| 32 | 103.5 | 5.5 | 399 | 7 | US-11-028-169-3323 Sequence 3323, Ap |
| 33 | 103.5 | 5.5 | 399 | 7 | US-11-028-204-3323 Sequence 3323, Ap |
| 34 | 103.5 | 5.5 | 399 | 7 | US-11-027-877-3323 Sequence 3323, Ap |
| 35 | 103.5 | 5.5 | 399 | 7 | US-11-027-879-3323 Sequence 3323, Ap |
| 36 | 103.5 | 5.5 | 399 | 7 | US-11-028-149-3323 Sequence 3323, Ap |
| 37 | 103.5 | 5.5 | 399 | 7 | US-11-027-802-3323 Sequence 3323, Ap |
| 38 | 103.5 | 5.5 | 399 | 7 | US-11-027-890-3323 Sequence 3323, Ap |
| 39 | 103.5 | 5.5 | 399 | 7 | US-11-027-892-3323 Sequence 3323, Ap |
| 40 | 103.5 | 5.5 | 399 | 7 | US-11-028-099-3323 Sequence 3323, Ap |
| 41 | 103.5 | 5.5 | 399 | 7 | US-11-028-197-3323 Sequence 3323, Ap |
| 42 | 103.5 | 5.5 | 399 | 7 | US-11-027-844-3323 Sequence 3323, Ap |
| 43 | 103.5 | 5.5 | 399 | 7 | US-11-028-050-3323 Sequence 3323, Ap |
| 44 | 103.5 | 5.5 | 399 | 7 | US-11-028-457-3323 Sequence 3323, Ap |
| 45 | 103.5 | 5.5 | 399 | 7 | US-11-027-891-3323 Sequence 3323, Ap |

ALIGNMENTS

```
RESULT 1
US-11-061-894-14
; Sequence 14, Application US/11061894
; GENERAL INFORMATION:
; APPLICANT: McCutchen, Billy F.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061, 894
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546, 845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546, 533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Solanum tuberosum
; US-11-061-894-14

Query Match      54.4% Score 1014; DB 7; Length 386;
Best Local Similarity 88.3%; Pred. No. 9e-76;
Matches 196; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 145 LGMVTVLSDGGGIRGIIIPATILFEELQLOEDMNNADARLADYDVIGTSTGILTA 204
    |||||
Db 25 LGMVTVLSDGGGIRGIIIPATILFEELQLOEDMNNADARLADYDVIGTSTGILTA 84
    |||||

QY 205 MISTPENNRPAAAEIYFFTEHGPQIFPNSGQILGPKYDKKYLMOYLQEKIETRYH 264
    |||||
Db 85 MITTPENNRPAAAEIYFFTEHGPQIFPNSGQILGPKYDKKYLMOYLQEKIETRYH 144
    |||||

QY 265 QALTEVVISFDIKTKKPVIFTKSNLANSPELDAAKMYDSYSTRAAPTYEPPHYFVNTS 324
    |||||
Db 145 QALTEVVISFDIKTKKPVIFTKSNLANSPELDAAKMYDSYSTRAAPTYEPPHYFVNTS 204
    |||||

QY 325 NGDEYEFNLVDGAVATVPDPAALISIVATRLAQDPAPASIR 366
    |||||
Db 205 NGATYEFNLVDGAVATVPDPAALISIVATRLAQDPAPASIR 246
    |||||

RESULT 2
US-11-061-894-10
; Sequence 10, Application US/11061894
; GENERAL INFORMATION:
```

```

; APPLICANT: McCutchen, Billy F.
; APPLICANT: Aad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061,894
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Pentaclethra macroloba
US-11-061-894-10

```

```

Query Match      28.3%; Score 528.5; DB 7; Length 408;
Best Local Similarity 53.1%; Pred. No. 1.1e-35;
Matches 113; Conservative 33; Mismatches 50; Indels 17; Gaps 7;

```

```

QY 146 GEMVTVLSIDGGIRGIIPTILFLESGOLEMNNADARLADYFDVIGSTGSLTAM 205
DB 33 GNLVTVLADGGIRGIIPTILFLESGOLEMNNADARLADYFDVIGSTGSLTAM 90
QY 206 ISTPNENN--RPPAAKEIVPFYFEHGPQIFNPSGQ-----ILGPKYDKYLMQVLOEKL 258
DB 91 LTAHPDQNDKRPVLYAAEEIIDFYIEHGPSIFNKSTACSLGIPCKDKGKYLQELISQKL 150
QY 259 GEFTRVQALTEVVISFSDIKTNKPVIFTKSNLNSPELDKMYDISYTAAPTYPPHY 318
DB 151 NETLLDQTTNNVIPSFDIKLARPTIFSTFKLEVEVELNVLKSDVCMGTSAAPIVPEPPY 210
QY 319 FVTNTSNGDEYEFNLVDGAVATVAD--PALLSIS 350
DB 211 F----KHGDT-EFNLVDGAI--IADIPAPVALS 236

```

```

RESULT 3
US-11-061-894-12
; Sequence 12, Application US/11061894
; GENERAL INFORMATION:
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Aad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061,894
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Lipase (codon optimized mopentin)
US-11-061-894-12

```

```

Query Match      28.3%; Score 528.5; DB 7; Length 408;
Best Local Similarity 53.1%; Pred. No. 1.1e-35;
Matches 113; Conservative 33; Mismatches 50; Indels 17; Gaps 7;

```

```

QY 146 GEMVTVLSIDGGIRGIIPTILFLESGOLEMNNADARLADYFDVIGSTGSLTAM 205
DB 33 GNLVTVLADGGIRGIIPTILFLESGOLEMNNADARLADYFDVIGSTGSLTAM 90

```

```

QY 206 ISTPNENN--RPPAAKEIVPFYFEHGPQIFNPSGQ-----ILGPKYDKYLMQVLOEKL 258
DB 91 LTAHPDQNDKRPVLYAAEEIIDFYIEHGPSIFNKSTACSLGIPCKDKGKYLQELISQKL 150
QY 259 GEFTRVQALTEVVISFSDIKTNKPVIFTKSNLNSPELDKMYDISYTAAPTYPPHY 318
DB 151 NETLLDQTTNNVIPSFDIKLARPTIFSTFKLEVEVELNVLKSDVCMGTSAAPIVPEPPY 210
QY 319 FVTNTSNGDEYEFNLVDGAVATVAD--PALLSIS 350
DB 211 F----KHGDT-EFNLVDGAI--IADIPAPVALS 236

```

```

RESULT 4
PCT-US05-07908-100
; Sequence 100, Application PC/TUS0507908
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: GRAMATIKOVA, Svetlana
; APPLICANT: HAZLEWOOD, Geoff
; APPLICANT: BARTON, Nelson
; APPLICANT: LAM, David
; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 56446-20042.49
; CURRENT APPLICATION NUMBER: PCT/US05/07908
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 10/796,907
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 10/421,654
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,313
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample.
PCT-US05-07908-100

```

```

Query Match      14.4%; Score 268.5; DB 1; Length 350;
Best Local Similarity 34.1%; Pred. No. 2.6e-14;
Matches 74; Conservative 45; Mismatches 73; Indels 25; Gaps 8;

```

```

QY 151 VLSIDGGIRGIIPTILFLESGOLEMNNADARLADYFDVIGSTGSLTAMISTPN 210
DB 6 ILSIDGGIRGIIPTILFLESGOLEMNNADARLADYFDVIGSTGSLTAMISTPN 59
QY 211 ENNRPPAA--KEIVPFYFEHGPQIF-----NPSQILGPKYDKYLMQVLOEKL 259
DB 60 PDDEETRACTPDLKLKYVDHGKIKFEKNPIILGNIPFG--LNDPRQPPDELNRKLAQIG 118
QY 260 ET-RVHQALTEVVISFSDIKTNKPVIFTKSNLNSPELDKMYDISYTAAPTYPPHY 318
DB 119 LFAITLDKGLTKVILYADYIQROALFMANTDMENS---NFRYEAARATSAAPTYPPAL 175
QY 319 FV-TNTSNGDEYEFNLVDGAVATVADPALLSISVATR 354
DB 176 IERVGRKNKDKRFVPLIDGV--FANDPILAAVYEAR 210

```

```

RESULT 5
PCT-US05-07908-18
; Sequence 18, Application PC/TUS0507908
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: GRAMATIKOVA, Svetlana
; APPLICANT: HAZLEWOOD, Geoff
; APPLICANT: BARTON, Nelson
; APPLICANT: LAM, David

```


QY 258 LGSTRVHQAALTEWISSPFIKTNK--PV--ITTKSNLANSPELDAK-----HYDYSSTAA 309
 DQ 106 LGNTKRLREISKRVLISSFDLDBERDPTKRSWTPTPFHNPFDIDBGEQLVAYKALYTSA 166
 QY 310 APTPTYPHVTNTSGDEYEFTNLV--GAVAVAPADALLISTSVANRLQAQKOPASR 366
 DQ 166 APTTYPF-----TVDS-----YIDGVVANNPSSMALAQOTDTRALCTPPRSEIR 210

RESULT 8

```

PCT-US05-07908-132
Sequence 132, Application PC/TUS0507908
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: GRAMATIKOVA, Svetlana
APPLICANT: HAZLEWOOD, Geoff
APPLICANT: BARTON, Nelson
APPLICANT: Lam, David
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 56446-30042.49
CURRENT APPLICATION NUMBER: PCT/US05/07908
CURRENT FILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: 10/796,907
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: 10/421,654
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,313
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 132
LENGTH: 308
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (11)...(194)
OTHER INFORMATION: Patatin-like phospholipase
PCT-US05-07908-132

```

[illegible]

RESULT 9
PCT-US05-07908-36

```

: Sequence 36, Application PC/TUS05079008
:
: GENERAL INFORMATION:
:
: APPLICANT: DIVERSA CORPORATION
:
: APPLICANT: GRAMATIKOVA, Svetlana
:
: APPLICANT: HAZLEWOOD, Geoff
:
: APPLICANT: BARTON, Neilson

```

```

? APPLICANT: LAM, David
? TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM
? TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
? FILE REFERENCE: 56446-20042.49
? CURRENT APPLICATION NUMBER: PCT/US05/07908
? CURRENT FILING DATE: 2005-03-08
? PRIOR APPLICATION NUMBER: 10/796,907
? PRIOR FILING DATE: 2004-03-08
? PRIOR APPLICATION NUMBER: 10/421,654
? PRIOR FILING DATE: 2003-04-21
? PRIOR APPLICATION NUMBER: 60/374,313
? PRIOR FILING DATE: 2002-04-19
? NUMBER OF SEQ ID NOS: 174
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 36
? LENGTH: 462
? TYPE: PRT
? ORGANISM: Unknown
? FEATURE:
? OTHER INFORMATION: Obtained from an environmental sample.
PCT-US05-07908-36

```

| | | | | |
|-----------------------|--------|--------------------|-------|-----------------------------------|
| Query Match | 8.8%; | Score 165; | DB 1; | Length 462; |
| Best Local Similarity | 25.6%; | Prod. No. 1,3e-05; | | |
| Matches | 57; | Conservative | 44; | Mismatches 90; Indels 32; Gaps 8; |

| | | | |
|----|-----|--|-----|
| QY | 151 | VLSIDGGGIRGIIIPATILLEFLGEOLOEMDNNDARLADYDPVIGTGTGGLITLMISTPN | 210 |
| | | | |
| Db | 28 | ILALDDGGVGGAASVAFLEIRIAVL--EARLGRKYLGHWFLELIGTGTGALIGALMG- | 85 |
| | | | |
| QY | 211 | ENNRPPAAAKEIPEYFEHGPOLP--NPSGOI--LGP---KVDGKYLQVLOEKLGETRVH | 264 |
| | | | |
| Db | 86 | -----FAADVDORFTHELAPRVPRHLLIGLILRPFAKFDARLLAEIRITIGDSILG | 139 |
| | | | |
| QY | 265 | QALTEVVISFPIKTKNPVIFTKSNLNSP-----ELDAKMDISYSTAAAP | 311 |
| | | | |
| Db | 140 | D---KALMTGFALVAKMDGTSTWILLNNRSKRYWEGRDGVGNKDYLGLSLRASTAP | 196 |
| | | | |
| QY | 312 | TYRPPHFYFNTNSGDYEFN--LYDCAVATVADPALLSISVA | 352 |
| | | | |
| Db | 197 | LYDPDEEVVIAEARKDLEGIRGLFVDGQVDPHPNNPSLAMLILA | 239 |
| | | | |

RESULT 10
US-60-655

```

US-60-655-875-130981
: Sequence 130981, Application US/60655875
: GENERAL INFORMATION:
: APPLICANT: Boukharov, Andrey
: APPLICANT: Du, Zijing
: APPLICANT: Guo, Liang
: APPLICANT: Kovacic, David
: APPLICANT: Lu, Maolong
: APPLICANT: McCarter, James
: APPLICANT: Miller, Nancy
: APPLICANT: Williams, Deryck
: APPLICANT: Vaudin, Mark
: APPLICANT: Wu, Wei
: TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
: TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
: FILE REFERENCE: 38-21(53865)
: CURRENT APPLICATION NUMBER: US/60/655,875
: CURRENT FILING DATE: 2005-02-24
: NUMBER OF SEQ. ID NOS: 171306
: SEQ ID NO 130981

```

OTHER INFORMATION: =80%, HitCoverage=37%, E-value=3e-36, Identity=36%, Hit description: OTHER INFORMATION: =similar to CG6718-PB [Apis mellifera]
US-60-655-875-130981

Query Match 8.3%; Score 154; DB 8; Length 364;
Best Local Similarity 27.7%; Pred. No. 7.7e-05;
Matches 74; Conservative 37; Mismatches 92; Indels 64; Gaps 14;

73 VOENALGGTTEMDASEANMELLVOGENLTKKPSVEDNPETYEAL-KRPAFLDSDRK 131
24 VLEKKTGTSE-----ESTVKKPECCD---VEEAIWEMQOM---AL 60
132 KLRANKASYPGQUGENVTVLSDGGIRGIIPTILFELEGQLOEMDNADRLADY-- 189
61 KTRRNKQKTPBRKGTGVRALSLDGGIRGVLYQVLMEMSLAVGEGLOAGHEKNFVQ 120
190 --FDVIGTSTGGLLT-AMISTPENNRPPAAKEIVPFYFEGHQIPNSGQILGPKYD 246
121 KNFNWIIIGTSTGVALVALVSG-----ISLIDARLYRLKDSVFGARAQLIG--YN 170
247 GKLYMQVLQKLGRTVHQALTEVVISFDIKTKNPVIFTKSN-LANSPELDACM----- 300
171 AQNLFFFLQAFGE--NKKMAE--LSRGNIKGLKIGLFTATYVQKPPRLVFRNPFIS 225
301 -----YD-----ISYTAAPTYF 314
226 ALNEYDPYKTNIMWLAARYST-AAPTYF 251

RESULT 11

US-11-061-233-8
Sequence 8, Application US/11061233
GENERAL INFORMATION:
APPLICANT: McCutchen, Billy F.
APPLICANT: Adad, Andre R.
APPLICANT: Wong, James F.
APPLICANT: Yu, Guo Cao
TITLE OF INVENTION: Lipases and Methods of Use
FILE REFERENCE: 035718/286811
CURRENT APPLICATION NUMBER: US/11/061,233
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: 60/546,605
PRIOR FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 314
TYPE: PRT
ORGANISM: Nitrosomonas europaea
US-11-061-233-8

Query Match 7.9%; Score 146.5; DB 7; Length 314;
Best Local Similarity 24.3%; Pred. No. 0.00026;
Matches 55; Conservative 46; Mismatches 92; Indels 33; Gaps 10;

142 PGQUGENVTVLSDGGIRGIIPTILFELEGQLOEMDNADRLADYFDVIGTSTGGL 201
7 PG-ASALLRVLTLDDGGAKGP-----YTLGVKKEIEAWVGCPLHOKFDFVETSTGAI 58
202 LTMISTPENNRPPAAKEIVPFYFEGHQIPNSGQILGPKYDKYLMQVLOEKLGRT 261
59 IASIALGH-----SVDSILEYRKHVPTWS--QKRAPA-RSQALKKLASVEVGDA 107
262 RVHQALTEVVISFDIKTKNPVIFTKSNLANS-----PELDKMYDISYSTAAPTY 313
108 TFSQVKTGIGIVTAKWTERPMIF-KGSVAQAHGQVTFVPGFVSIALDAVKASCSAYPF 166
314 PPHYFVPTNSNGDEVEFNVDGAVATVADPALISIVARRLAKD 359
167 F--ERTVRTSMGSDIE--LIDGGYC-ANNPTLYALADAVQALRSD 207

RESULT 12

US-11-061-894-8
Sequence 8, Application US/11061894
GENERAL INFORMATION:

APPLICANT: McCutchen, Billy F.
APPLICANT: Adad, Andre R.
TITLE OF INVENTION: Methods for Enhancing Insect Resistance
FILE REFERENCE: 035718/286812
CURRENT APPLICATION NUMBER: US/11/061,894
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: 60/546,845
PRIOR FILING DATE: 2004-02-23
PRIOR APPLICATION NUMBER: 60/546,533
PRIOR FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 314
TYPE: PRT
ORGANISM: Nitrosomonas europaea
US-11-061-894-8

Query Match 7.9%; Score 146.5; DB 7; Length 314;
Best Local Similarity 24.3%; Pred. No. 0.00026;
Matches 55; Conservative 46; Mismatches 92; Indels 33; Gaps 10;

142 PGQUGENVTVLSDGGIRGIIPTILFELEGQLOEMDNADRLADYFDVIGTSTGGL 201
7 PG-ASALLRVLTLDDGGAKGP-----YTLGVKKEIEAWVGCPLHOKFDFVETSTGAI 58
202 LTMISTPENNRPPAAKEIVPFYFEGHQIPNSGQILGPKYDKYLMQVLOEKLGRT 261
59 IASIALGH-----SVDSILEYRKHVPTWS--QKRAPA-RSQALKKLASVEVGDA 107
262 RVHQALTEVVISFDIKTKNPVIFTKSNLANS-----PELDKMYDISYSTAAPTY 313
108 TFSQVKTGIGIVTAKWTERPMIF-KGSVAQAHGQVTFVPGFVSIALDAVKASCSAYPF 166
314 PPHYFVPTNSNGDEVEFNVDGAVATVADPALISIVARRLAKD 359
167 F--ERTVRTSMGSDIE--LIDGGYC-ANNPTLYALADAVQALRSD 207

RESULT 13

US-60-655-875-139557
Sequence 139557, Application US/60655875
GENERAL INFORMATION:

APPLICANT: Boukharov, Andrey
APPLICANT: Du, Zijing
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Lu, Maolong
APPLICANT: McCarter, James
APPLICANT: Miller, Nancy
APPLICANT: Williams, Deryck
APPLICANT: Vaudin, Mark
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 139557
LENGTH: 239
TYPE: PRT
ORGANISM: Heterodera glycines

OTHER INFORMATION: Coding regions on vcdna: vcdna-SeqID 65980; Strand++; Position=1
OTHER INFORMATION: -78,643-849,1362-1475,1684-1826,2183-2358
FEATURE:
OTHER INFORMATION: Homolog annotation: Hit ID=XP_394049.1; Match level="QueryCoverage
OTHER INFORMATION: =68%, HitCoverage=21%, E-value=4e-20, Identity=35%"; Hit description:

```
; OTHER INFORMATION: =similar to CG6718-PB [Apis mellifera]
US-60-655-875-139557
Query Match
Best Local Similarity 25.3%; Pred. No. 0.0012;
Matches 64; Conservative 37; Mismatches 95; Indels 57; Gaps 10;
QY 73 VQENALTGTTTMDSDASEANMELLVOYGENILKKPVSNDPEYEEAL-KRAKLSDRK 131
DB 24 VLEKKKTGTGKSE-----ESTVKKPEKCV-----VEBALMKEMQOM--AL 60
QY 132 KLAANKASYGPGQGENYTVLSIDGGIRGIIIPATIEFLEGQEDNNADARADY-- 189
DB 61 KTRNEKRTKPTRTGNGVRALSIDGGIRGIVLVQMLIEMSLYGEGLQAGHEKXEVQ 120
QY 190 --PDVIGTSTGGLT-AMISTPENNRPPAAKEIYFPEHGPQIFNPGQILGPYD 246
DB 121 KKNWITIGTGTALVALALVSG-----TSLDALRLRLKDSVFGARQLIG--YN 170
QY 247 GKYLMOVLQEKLGTRVHQALETEVIVSSFDIKTKRPVIFTK-----SNLANSPELDAMY 301
DB 171 AQNLFTFLQALFTTATYVG-----QKPRVLVKFRNFTSDLMEVNPYKTNIV 217
QY 302 DISYSTAAATYF 314
DB 218 LAARYSSAAPTYP 230

RESULT 14
US-60-655-875-127287
; Sequence 127287, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Kovalic, David
; APPLICANT: Luo, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655, 875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 127287
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID.53710; Strand=-; Position=1
; OTHER INFORMATION: -129,619-750,1035-1159,1403-1560,1608-1656,1896-1929,1992-2066,21
; OTHER INFORMATION: -2186
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=NP_872170.1; Match level="QueryCoverag
; OTHER INFORMATION: =91%, HitCoverage=24%, E-value=6e-57, Identity=45%, Hit descrip
; OTHER INFORMATION: =anhytin and petatin family member (SVI186) [Caenorhabditis elegat
; OTHER INFORMATION: emb|CAD54162.1| Hypothetical protein W
US-60-655-875-127287
Query Match
Best Local Similarity 7.2%; Score 133.5; DB 8; Length 258;
Matches 56; Conservative 39; Mismatches 59; Indels 79; Gaps 12;
QY 114 EYEBALKRPAKLSDRKURANKASYGPGQGENYTVLSIDGGIRGIIIPATIEFLEG 173
DB 1 DIVDEVLDKUPVSSD-----DTPPDH--NFIVVLSIDGGIRGLVLIQILIVER 50
QY 174 QLOEMDNADARLADYFDVIGTSTGGLT--AMISTPENNRPPAAKEIYFPEYE-- 228
```

```
DB 51 IME-----PIFPFDWVGSTGANTAGLACQTHOURLYRKEDWV---FDR 100
QY 229 --HGQIFNPGQILGPKYDGKYLMOVLQEKLGTRVHQALETEVIVSSFDIKTKRPVIF 286
DB 101 RPHNTQV-----LEKFIROEMQ-----AETMPS--DLKPR-LMFT 133
QY 287 KSNLA-----NSPELDARKYDISYST-----AAAPTYP 314
DB 134 TTRAEFPVOLKIMRNKYKLPTEDENEBELGYRTPDDLMLKVLRRSSAAPTYP 186

RESULT 15
US-11-045-874-10
; Sequence 10, Application US/11045874
; GENERAL INFORMATION:
; APPLICANT: Georgia Tech Research Corporation
; TITLE OF INVENTION: Methods and Compositions for NAD (P) (H) Oxidases
; FILE REFERENCE: GTRC130PCT
; CURRENT APPLICATION NUMBER: US/11/045, 874
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: PCT/US03/24067
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/399, 850
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-045-874-10
Query Match
Best Local Similarity 21.0%; Score 113; DB 7; Length 444;
Matches 100; Conservative 53; Mismatches 113; Indels 210; Gaps 25;
QY 4 YKKMLLSLGT-----GTTSEFDKTYTAKAATWTAVHMLVIOQM 44
DB 32 YEKTNIVSFGTGLPYPVGGFPDNPNTWISRTQEBEFTKGIS----- 73
QY 45 TDAASVTMDYISTFQAL--DSKNYIARVQENALGTGTTTMDSDASEANMELLVOYGEN 102
DB 74 -----YKTHBAIKYDANKNTI-VINQKTGYI-----FNNTYDQIMATGAK 115
QY 103 LKKPVSNDPEYEEALKRF-----AKLSDRKURANKASYGPGQLG----- 146
DB 116 PTPPTNNINLENF-HTLKNLEDEGQIKKLMDBREIK-NIALLGGYIGIEMVEAAKAKR 173
QY 147 -----EMVTVLISID-----GGGI----- 159
DB 174 KVRRLQLDKHLIDSFDEIVYIMEBELTKGVNLHTNMFVKSILGEKKAGGVNTKNT 233
QY 160 -----RGITPATILSFLEGQLOEMDNADARLADYFDVIGTSTGGLTA----- 204
DB 234 YQDAVILATGICPDD--EFLNQLTTRKGA-IIVNEY---GETSIRKINISAGDCAT 286
QY 205 --MISTPENNRPPAAKEIYFPEHGPQIFNPGQILGPKYDGKYLMOVLQEKLGTR 262
DB 287 YNIVSKKNB-YIPLATTA-----NKLGRIVGENLAGN----- 317
QY 263 VHQALTEVIVSSFDIKTKRPVIFTKSNLANSPELDARKYDISYSTAAATYPPEHYFV-- 320
DB 318 -HTAF-KGTIGASIK-----LSLEAARGLTEKAKRQIKKT-----LFVVD 361
QY 321 ---TNTSNGD-----YEFN--LYDGAVALYADPAL-----LSISVATRLAQD 359
DB 362 KNTNTYYPGQEDLYIKLIYEENKTIILGAQATGKNGAVWRHIALSTAIYSKLTKE 417

Search completed: April 8, 2005, 08:06:45
Job time : 39 secs
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